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SESSION RESUMED IN FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS'
AT 12:15:44 ON 11 MAR 2005
FILE 'MEDLINE' ENTERED AT 12:15:44 ON 11 MAR 2005
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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                         ENTRY    SESSION
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=> d his

     (FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11
     MAR 2005
L1             0 INITIAT? (W) DNA (W) UPTAKE
L2           373 INITIAT? (S) DNA (S) UPTAKE
L3          4746 NON (W) HOMOLOGOUS
L4             0 L2 AND L3
L5           209 STUFFER AND DNA
L6             0 L5 AND L2
L7          2254 DNA (W) UPTAKE
L8             1 L7 AND L3
L9             0 L5 AND L7
L10        18629 DNA (S) UPTAKE
L11            0 L10 AND L5
L12            7 L10 AND L3
L13            4 DUP REM L12 (3 DUPLICATES REMOVED)
                 E DIAZ (W) TORRES MARIA/AU
                 E DIAZ TORRES MARIA/AU
L14           54 E1-E4
L15           23 DUP REM L14 (31 DUPLICATES REMOVED)
L16            2 TRANSFORM? AND L15
L17            0 L3 AND L5
L18      1447160 TRANSFORM?
L19          470 L3 AND L18
L20            0 L19 AND L5
L21            5 L19 AND L10
L22            2 DUP REM L21 (3 DUPLICATES REMOVED)
```

R: AT BE CH DE DK ES FR GB IT LI NL SE
JP 06509942 W 19941110 (199504)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9304180	A1	WO 1992-EP1878	19920818
EP 599945	A1	EP 1992-917882	19920818
		WO 1992-EP1878	19920818
JP 06509942	W	WO 1992-EP1878	19920818
		JP 1993-504107	19920818

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 599945	A1 Based on	WO 9304180
JP 06509942	W Based on	WO 9304180

PRIORITY APPLN. INFO: DE 1991-4127669 19910822
AN 1993-094010 [11] WPIDS
AB WO 9304180 A UPAB: 19931122
Claimed is the purposive genetic modification of the hemi ascomycete Ashbya (A.) gossypii by **transforming** A. gossypii with vectors containing the DNA to be introduced **flanked** by one or more gene regions of A. gossypii.

Pref. the gene regions are derived from the translation elongation factor TEF) 1-, and the vectors are plasmid pAG-102 or pAG-145 or derivs. thereof.

Also claimed is genetically modified A. gossypii, pref. A. gossypii strains LU8334 to LU8341 (DSM 6661-6668).

USE/ADVANTAGE - A. gossypii may be used in riboflavin production DNA from, e.g. Saccharomyces (S.) cerevisiae, Bacillus subtilis or E. coli can stably be **transformed** into and amplified in A. gossypii. The rate of homologous recombination compared to **non-homologous** recombination occurring naturally is increased allowing the purposive modification of A. gossypii
Dwg.0/15

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

L1	0	INITIAT? (W) DNA (W) UPTAKE
L2	373	INITIAT? (S) DNA (S) UPTAKE
L3	4746	NON (W) HOMOLOGOUS
L4	0	L2 AND L3
L5	209	STUFFER AND DNA
L6	0	L5 AND L2
L7	2254	DNA (W) UPTAKE
L8	1	L7 AND L3
L9	0	L5 AND L7
L10	18629	DNA (S) UPTAKE
L11	0	L10 AND L5
L12	7	L10 AND L3
L13	4	DUP REM L12 (3 DUPLICATES REMOVED)
		E DIAZ (W) TORRES MARIA/AU
		E DIAZ TORRES MARIA/AU

FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:39:56 ON 11 MAR 2005

L23 33 CONSTRUCT AND L19
L24 19 DUP REM L23 (14 DUPLICATES REMOVED)
L25 63 FLANK? AND L19
L26 27 DUP REM L25 (36 DUPLICATES REMOVED)
L27 6 L24 AND L26
L28 21 L26 NOT L27

=> heterologous
L29 133659 HETEROLOGOUS

=> l29 and l18
L30 14048 L29 AND L18

=> (construct or flank?) and l30
L31 1925 (CONSTRUCT OR FLANK?) AND L30

=> l5 and l31
L32 3 L5 AND L31

=> dup rem l32
PROCESSING COMPLETED FOR L32
L33 3 DUP REM L32 (0 DUPLICATES REMOVED)

=> t ti l33 1-3

L33 ANSWER 1 OF 3 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI New transactivation system having genetically **transformed** cells of the host plant with inactive or silenced foreign nucleic acid sequence and recombinant RNA viral vector, useful in producing a foreign polypeptide of interest.

L33 ANSWER 2 OF 3 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Producing **transformed** microorganism, preferably Bacillus, involves selecting competent microorganism, producing **DNA construct** in vitro, and directly **transforming** the microorganism with the **DNA construct**.

L33 ANSWER 3 OF 3 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Novel adenoviral vectors and helper viruses, useful for **transforming** cells and in genetic and nucleic acid vaccines.

=> d ibib abs l33 1-3

L33 ANSWER 1 OF 3 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-420305 [39] WPIDS
DOC. NO. CPI: C2004-157857
TITLE: New transactivation system having genetically **transformed** cells of the host plant with inactive or silenced foreign nucleic acid sequence and recombinant RNA viral vector, useful in producing a foreign polypeptide of interest.
DERWENT CLASS: C06 D16
INVENTOR(S): HULL, A; METT, V; SKARJINSKAIA, M; YUSIBOV, V
PATENT ASSIGNEE(S): (FRAU-N) FRAUNHOFER USA
COUNTRY COUNT: 107
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004044161	A2	20040527	(200439)*	EN	49
RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
AU 2003287622	A1	20040603	(200470)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004044161	A2	WO 2003-US35869	20031106
AU 2003287622	A1	AU 2003-287622	20031106

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2003287622	A1 Based on	WO 2004044161

PRIORITY APPLN. INFO: US 2003-465474P 20030425; US 2002-424275P 20021106

AN 2004-420305 [39] WPIDS

AB WO2004044161 A UPAB: 20040621

NOVELTY - Transactivation system for producing a foreign polypeptide of interest in host plant cells comprises:

(1) genetically **transformed** host plant cells having integrated in their nuclear genome, an inactive or silenced foreign nucleic acid sequence; and

(2) a recombinant RNA viral vector capable of infecting the cells of the host plant and encoding a factor for activating or facilitating the expression of inactive or silenced foreign nucleic acid sequence.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for producing a foreign polypeptide in cells of a host plant.

USE - The transactivation system is useful for producing a foreign polypeptide of interest in cells of a host plant (claimed).

Dwg.0/14

L33 ANSWER 2 OF 3 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2002-269188 [31] WPIDS

DOC. NO. CPI: C2002-079914

TITLE: Producing **transformed** microorganism, preferably Bacillus, involves selecting competent microorganism, producing **DNA construct** in vitro, and directly **transforming** the microorganism with the **DNA construct**.

DERWENT CLASS: B04 D16

INVENTOR(S): DIAZ-TORRES, M R; LEE, E W; MORRISON, T B; SCHELLENBERGER, V; SELIFONOVA, O V

PATENT ASSIGNEE(S): (GEMV) GENENCOR INT INC; (DIAZ-I) DIAZ-TORRES M R; (LEEE-I) LEE E W; (MORR-I) MORRISON T B; (SCHE-I) SCHELLENBERGER V; (SELI-I) SELIFONOVA O V

COUNTRY COUNT: 97

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2002014490 A2 20020221 (200231)* EN 48
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2001079254 A 20020225 (200245)
US 2002182734 A1 20021205 (200301)
EP 1309677 A2 20030514 (200333) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002014490	A2	WO 2001-US25166	20010810
AU 2001079254	A	AU 2001-79254	20010810
US 2002182734	A1 Provisional	US 2000-224948P	20000811
		US 2001-927161	20010810
EP 1309677	A2	EP 2001-957519	20010810
		WO 2001-US25166	20010810

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2001079254	A Based on	WO 2002014490
EP 1309677	A2 Based on	WO 2002014490

PRIORITY APPLN. INFO: US 2000-224948P 20000811; US 2001-927161 20010810

AN 2002-269188 [31] WPIDS

AB WO 200214490 A UPAB: 20020516

NOVELTY - Producing (M1) a **transformed** microorganism, preferably Bacillus, involves selecting a competent microorganism, producing a **DNA construct** in vitro, and directly **transforming** the microorganism with the **DNA construct** such that the **DNA construct** becomes integrated into a chromosome of the microorganism.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a library of mutants (I) produced by M1;

(2) directed evolution (M2) of a sequence in the host cell chromosome, involves in vitro mutagenesis of a **DNA construct**, direct **transformation** of the mutagenized sequence into a competent host cell, screening for, or selection of, mutants possessing or exhibiting a desired property, and repeating the above mentioned steps for one or more rounds; and

(3) constructing (M3) a sequence of interest at a target sequence of a selected microorganism, where the target sequence includes a residing marker, involves assembling a **DNA construct** in vitro comprising an incoming sequence, a selectable marker, and two **flanking** sequences which are homologous to sequences of the target sequence, where the selectable marker of the **DNA construct** is different than the residing marker of the microorganism, **transforming** the microorganism with the **DNA construct** under conditions permitting the incoming sequence and selectable marker to inactivate the residing marker, and selecting for **transformants** that include the selectable marker,

and repeating the above mentioned steps, where with each repetition of the **DNA construct** comprises a selectable marker different from the selectable marker in the previous step and the selectable marker of the previous step acts as the residing marker in the microorganisms.

USE - M1 is useful for producing a **transformed** microorganisms selected from Acinetobacter, Thermus, Deinococcus, Radiodurans, and Bacillus, preferably Bacillus, where the Bacillus is a super-competent strain, preferably a Pxyl-comK strain (claimed).

ADVANTAGE - M1 **transforms** the **DNA** constructs into the microorganism with good efficiency, and allows for the generation of large libraries. M1 provides in vitro construction and direct **transformation** into Bacillus, without the use of any intervening microorganisms. M1 does not require antibiotic or other selectable marker to maintain the plasmid in the cells, which is undesirable for production strains and constrains choice of screening conditions. M1 allows evolution of single copy genes of a strain, and prevents variations in copy number which skews a library.

Dwg.0/15

L33 ANSWER 3 OF 3 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2000-543486 [49] WPIDS
CROSS REFERENCE: 2000-558402 [51]
DOC. NO. CPI: C2000-161741
TITLE: Novel adenoviral vectors and helper viruses, useful for **transforming** cells and in genetic and nucleic acid vaccines.
DERWENT CLASS: B04 D16
INVENTOR(S): BETT, A; SANDIG, V; YOUIL, R
PATENT ASSIGNEE(S): (MERI) MERCK & CO INC
COUNTRY COUNT: 22
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000046360	A1	20000810	(200049)*	EN	107
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
EP 1151091	A1	20011107	(200168)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
JP 2002535986	W	20021029	(200274)		120

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000046360	A1	WO 2000-US2405	20000131
EP 1151091	A1	EP 2000-910029	20000131
		WO 2000-US2405	20000131
JP 2002535986	W	JP 2000-597420	20000131
		WO 2000-US2405	20000131

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 1151091	A1	Based on	WO 2000046360
JP 2002535986	W	Based on	WO 2000046360

PRIORITY APPLN. INFO: US 1999-138134P 19990608; US 1999-118601P 19990204

AN 2000-543486 [49] WPIDS
CR 2000-558402 [51]

AB WO 200046360 A UPAB: 20021118
NOVELTY - Nucleic acid molecule (I) comprising a low homology packaging signal cassette (a modified adenovirus packaging signal with low homology to a wild-type adenovirus packaging signal) **flanked** by a recombinase recognition sequence, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a nucleic acid comprising an adenovirus E3 gene with a 2.7 kb insertion that does not contain a promoter sequence;

(2) an adenoviral helper virus for the production of helper dependent vectors comprising:

(a) an adenovirus genome with an E1 region deletion;

(b) an excisable packaging signal cassette (in place of a wild-type signal) comprising a 5' loxP site, a modified packaging signal and a 3' loxP site where the modified signal has low homology to and is less efficient that the wild type signal; and

(c) an optional insertion element comprising at least 2900 base pairs (bp) of non-adenoviral **DNA** inserted in the E3 region (without E3 region deletions);

(3) a vector comprising the adenovirus of (2);

(4) a cell line expressing E1 and infected with the virus of (2);

(5) a helper-dependent adenovirus vector of 28-36 kilo bases (kb) comprising:

(a) a 5' inverted terminal repeat (ITR);

(b) a packaging signal;

(c) at least 1 **heterologous** expression cassette;

(d) a human genomic **stuffer DNA**;

(e) an optional E4 non-coding segment conferring a selective advantage where the E4 element is located between nucleotide -400 from the right end; and

(f) a 3' ITR, where the only adenoviral sequences present are the ITR's, optional E4 segment and the packaging signal and no bacterial origin of replication or marker genes are present;

(6) a plasmid vector comprising:

(a) a 5' ITR;

(b) a packaging signal;

(c) at least 1 **heterologous** expression cassette;

(d) a human genomic **stuffer DNA**;

(e) an optional E4 non-coding segment conferring a selective advantage where the E4 element is located between nucleotide -400 from the right end; and

(f) a 3' ITR;

(7) a helper-dependent adenovirus that does not encode proteins needed for viral generation, is 28-36 kb long and is 50-60 % GC, comprising (5'-3');

(a) an ITR;

(b) a packaging signal directly joined 3' of the 5' ITR;

(c) a **DNA stuffer** of at least 1 kb;

(d) at least 1 **heterologous** expression cassette;

(e) a second **DNA stuffer** of at least 1 kb;

(f) an optional E4 non-coding segment of at least 400 bp; and

(g) an ITR (directly joined to the 5' end of the E4 segment, if present);

(8) generating helper-dependent adenoviral gene vectors in a cell line expressing E1 and cre recombinase comprising:

(a) infecting the cell line with a helper-dependent vector as in (5); and

(b) infecting the cell line with a helper virus as in (2); and

(c) obtaining the generated helper-dependent viral vectors; and

(9) generating a helper-dependent adenoviral vector that does not encode any adenoviral proteins, is 28-36 kb and 50-60 % CG, comprising:

(a) producing a cell comprising:

(i) trans functions needed for adenovirus generation; and
(ii) the helper-dependent adenoviral vector comprising the cis functions needed for adenovirus generation and at least 1 heterologous expression cassette; and
(b) generating the vector.
USE - The vectors are useful for the delivery of nucleic acids, e.g. for gene and nucleotide vaccines, and as transformation vectors. The cell line is useful for the production of the vectors.
DESCRIPTION OF DRAWING(S) - The diagram shows the structure of different helper-dependent adenoviral vectors.
Dwg.4/7

```
=> d his

     (FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11
     MAR 2005
L1             0 INITIAT? (W) DNA (W) UPTAKE
L2           373 INITIAT? (S) DNA (S) UPTAKE
L3          4746 NON (W) HOMOLOGOUS
L4             0 L2 AND L3
L5           209 STUFFER AND DNA
L6             0 L5 AND L2
L7          2254 DNA (W) UPTAKE
L8             1 L7 AND L3
L9             0 L5 AND L7
L10        18629 DNA (S) UPTAKE
L11            0 L10 AND L5
L12            7 L10 AND L3
L13            4 DUP REM L12 (3 DUPLICATES REMOVED)
                 E DIAZ (W) TORRES MARIA/AU
                 E DIAZ TORRES MARIA/AU
L14           54 E1-E4
L15           23 DUP REM L14 (31 DUPLICATES REMOVED)
L16            2 TRANSFORM? AND L15
L17            0 L3 AND L5
L18      1447160 TRANSFORM?
L19          470 L3 AND L18
L20            0 L19 AND L5
L21            5 L19 AND L10
L22            2 DUP REM L21 (3 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:39:56 ON 11
     MAR 2005
L23           33 CONSTRUCT AND L19
L24           19 DUP REM L23 (14 DUPLICATES REMOVED)
L25           63 FLANK? AND L19
L26           27 DUP REM L25 (36 DUPLICATES REMOVED)
L27            6 L24 AND L26
L28           21 L26 NOT L27
L29       133659 HETEROLOGOUS
L30        14048 L29 AND L18
L31         1925 (CONSTRUCT OR FLANK?) AND L30
L32            3 L5 AND L31
L33            3 DUP REM L32 (0 DUPLICATES REMOVED)

=> homologous 5n (flank or stuffer)
MISSING OPERATOR '5N (FLANK'
```

The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> homologous (5n) (flank or stuffer)
L34 63 HOMOLOGOUS (5N) (FLANK OR STUFFER)

=> l31 and l34
L35 4 L31 AND L34

=> dup rem l35 1-4
'1-4' IS NOT VALID. VALID FILE NAMES ARE 'WPIDS'
You have entered a file name of duplicates to keep that is not
referenced by any of the L#s specified for this DUPLICATE command.
The file names of duplicates that can be kept are listed above.
Please enter one of these file names.

=> dup rem l35
PROCESSING COMPLETED FOR L35
L36 4 DUP REM L35 (0 DUPLICATES REMOVED)

=> t ti l36 1-4

L36 ANSWER 1 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Preparation of eukaryotic cells negative for dihydrofolate reductase, useful, after **transformation**, for optimized production of selected proteins, by homologous recombination.

L36 ANSWER 2 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI New purified nucleic acid segment, useful for polymer grafting and the production of non-naturally occurring chimeric polymers, comprises a region encoding enzymatically active heparin synthase.

L36 ANSWER 3 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI New chondroitin synthase gene obtained from Pasteurella multocida, useful as hyaluronan polysaccharide substitute in medial or cosmetic applications, e.g. for eye or joint applications, for moisturizer or wound dressings.

L36 ANSWER 4 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Removing target nucleic acid sequences e.g. selectable marker genes, genes involved in plant cell metabolism, growth development and fertility from plastid genomes, by Cre-mediated site specific recombination.

=> d ibib abs l36 1-4

L36 ANSWER 1 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-702095 [69] WPIDS
CROSS REFERENCE: 1999-304823 [26]; 2000-001161 [01]
DOC. NO. CPI: C2004-248297
TITLE: Preparation of eukaryotic cells negative for dihydrofolate reductase, useful, after **transformation**, for optimized production of selected proteins, by homologous recombination.
DERWENT CLASS: B04 D16
INVENTOR(S): HOLTSCHKE, T; HONOLD, K; STERN, A
PATENT ASSIGNEE(S): (HOFF) ROCHE DIAGNOSTICS GMBH
COUNTRY COUNT: 24
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

EP 1464705 A1 20041006 (200469)* GE 34
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MK NL PT RO SE SI

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1464705	A1 Div ex	EP 1998-122807	19981201
	Div ex	EP 1999-112607	19981201
		EP 2004-6966	19981201

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1464705	A1 Div ex	EP 919619
	Div ex	EP 957165

PRIORITY APPLN. INFO: EP 1997-121075 19971201
AN 2004-702095 [69] WPIDS
CR 1999-304823 [26]; 2000-001161 [01]
AB EP 1464705 A UPAB: 20041027
NOVELTY - Preparing dihydrofolate reductase (DHFR)-negative eukaryotic cells (A), is new.

DETAILED DESCRIPTION - Preparing dihydrofolate reductase (DHFR)-negative eukaryotic cells (A) comprises:

(1) transfecting the cells with a vector that comprises at least one target sequence (TS) for a site-specific recombinase; sequences that **flank** TS and are **homologous** to a DHFR sequence endogenously present in the cell, to permit homologous recombination (HR); and optionally positive and/or negative selection marker genes (MG);

(2) growing the transfected cells under conditions suitable for HR; and

(3) recovering the resulting cells.

INDEPENDENT CLAIMS are also included for:

(1) introducing a **heterologous** DHFR gene into a eukaryotic cell;

(2) vector (V1) containing a sequence (X) that consists of an optional positive selection MG, sequence encoding DHFR and sequence encoding a desired protein, in expresssible form, where (X) is **flanked** by at least one TS;

(3) vector (V2) for HR containing a sequence (Y) that consists of an optional positive selection MG, **flanked** by at least one TS, also sequences that **flank** (Y) and are **homologous** with a DHFR sequence endogenously present in the cell, to permit HR, optionally also a negative selection MG, outside the **flanking** sequences;

(4) eukaryotic, preferably human, cells in which at least one endogenous DHFR-encoding sequence has been inactivated and, in this region, at least one TS has been integrated into the genome; and

(5) eukaryotic, preferably human, cells that have a **heterologous** nucleic acid sequence (Z) in the region of an endogenous DHFR locus, where (Z) contains sequences encoding DHFR and a desired protein, also at least one TS.

USE - (A) are transfected with a vector that contains a DHFR-coding sequence and a sequence that encodes a protein of interest (PI), and can then be used for optimized expression of PI, by gene amplification.
Dwg.0/8

L36 ANSWER 2 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-129159 [12] WPIDS
CROSS REFERENCE: 1999-337486 [28]; 2000-013032 [01]; 2000-376319 [32];

2003-066235 [06]; 2003-532558 [50]; 2003-755179 [71]; 2003-787045 [74]; 2003-787059 [74]; 2004-375496 [35]; 2004-709095 [69]

DOC. NO. CPI: C2003-032956

TITLE: New purified nucleic acid segment, useful for polymer grafting and the production of non-naturally occurring chimeric polymers, comprises a region encoding enzymatically active heparin synthase.

DERWENT CLASS: B04 D16

INVENTOR(S): DEANGELIS, P L

PATENT ASSIGNEE(S): (DEAN-I) DEANGELIS P L; (UYOK-N) UNIV OKLAHOMA

COUNTRY COUNT: 101

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002089742	A2	20021114	(200312)*	EN	128
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW					
US 2003099967	A1	20030529	(200337)		
EP 1392843	A2	20040303	(200417)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
AU 2002256501	A1	20021118	(200452)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2002089742	A2		WO 2002-US14581	20020508
US 2003099967	A1	Provisional	US 2001-289554P	20010508
		Provisional	US 2001-296386P	20010606
		Provisional	US 2001-303691P	20010706
		Provisional	US 2001-313258P	20010817
			US 2002-142143	20020508
EP 1392843	A2		EP 2002-725971	20020508
			WO 2002-US14581	20020508
AU 2002256501	A1		AU 2002-256501	20020508

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 1392843	A2	Based on	WO 2002089742
AU 2002256501	A1	Based on	WO 2002089742

PRIORITY APPLN. INFO: US 2001-313258P 20010817; US 2001-289554P 20010508; US 2001-296386P 20010606; US 2001-303691P 20010706; US 2002-142143 20020508

AN 2003-129159 [12] WPIDS

CR 1999-337486 [28]; 2000-013032 [01]; 2000-376319 [32]; 2003-066235 [06]; 2003-532558 [50]; 2003-755179 [71]; 2003-787045 [74]; 2003-787059 [74]; 2004-375496 [35]; 2004-709095 [69]

AB WO 200289742 A UPAB: 20041027

NOVELTY - A new purified nucleic acid segment (I) comprises a coding

region encoding enzymatically active heparin synthase, where the nucleic acid segment is capable of hybridizing to, or has a semiconservative or conservative amino acid changes or is a truncated segment when compared to, any of the fully defined sequences of 1851, 1854 or 1940 bp, given in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) A recombinant vector (II) consisting of a plasmid, cosmid, phage, integrated cassette or virus vector, where the recombinant vector further comprises (I);

(2) A recombinant host cell that is a prokaryotic cell **transformed** with (II), or is a eukaryotic cell transfected with (II), or is electroporated or **transformed** to introduce (II) into the recombinant host cell, or is transduced with a recombinant vector comprising a purified nucleic acid segment having a coding region encoding enzymatically active Pasturella multocida heparin synthase;

(3) A purified composition comprising a heparin polymer made by a recombinant process, heparin synthase, or by the Pasteurella multocida heparin synthase of a fully defined sequence of 617 or 651 amino acids or comprising the nucleotide sequences of 1851, 1854 or 1940 bp, given in the specification;

(4) A purified composition comprising a heparin polymer having a modified size distribution or structure;

(5) Producing (M1) a heparin polymer in vitro;

(6) A recombinant host cell containing a heparin synthase and an epimerase and/or at least one sulphotransferase;

(7) A composition comprising an enzymatically active heparin synthase polypeptide;

(8) Detecting (M2) a DNA species;

(9) Detecting (M3) a bacterial cell that expresses mRNA encoding Pasteurella multocida heparin synthase;

(10) Producing (M4) a heparin polymer;

(11) A pharmaceutical composition comprising a preselected pharmaceutical drug and a heparin polymer produced by a heparin synthase directly or after modification of the polymer by sulfation or epimerization or combinations;

(12) A purified and isolated nucleic acid sequence encoding enzymatically active heparin synthase, comprising:

(a) any of the fully defined sequence of 1851, 1854 or 1940 bp;

(b) complements of any of the sequences of (a); or

(c) sequences which will hybridize to the nucleic acid sequence of (a) or (b);

(13) A prokaryotic or eukaryotic host cell **transformed** or transfected with (I) or the nucleic acid of (14) to express heparin polymer in the host cell;

(14) An isolated nucleic acid segment consisting essentially of a nucleic acid segment encoding heparin synthase having at least one nucleic acid segment duplicative of (I) allowing possession of a biological property of encoding for a Pasteurella multocida heparin synthase;

(15) A cDNA sequence according to the nucleic acid segment of (14);

(16) A recombinant host cell that is a product of a process (M5);

(17) A recombinant method (M6) for producing a **heterologous** polypeptide in a host cell;

in vitro sulfation (M7) of a heparin polymer produced by a heparin synthase, where the polymer is sulfated by either chemical or enzymatic means;

(18) A polymer obtained by the process of epimerizing a heparin polymer produced by a heparin synthase;

(19) A recombinantly produced unsulfated heparin polysaccharide;

(20) A polysaccharide comprising alternating alpha 1,4-linked GlcNAc and beta 1,4-linked GlcUA in a 1:1 ratio;

(21) Producing a heparosan polymer;

(22) Producing a heparin polymer; and

(23) An amino acid sequence encoding a dual action enzymatically active heparin synthase, comprising the motif QTYXN(L/I)EX4DDX(S/T)D(K/N)(T/S)X6IAX(S/T)(S/T)(S/T)(K/R)V(K/R)X6NXGXYX16F QDXDDX(C/S)H(H/P)ERIXR, followed by the motif (K/R)DXGKFIX12-17DDDI(R/I)YPXDYX3MX45-55VNXLGTGTV

X = any amino acid residue and the parentheses encloses a subset of amino acid residues that may be present

USE - (I) is useful in methods of producing heparin synthase, a heparin and heparosan polymer. The methods are useful for detecting a DNA species, detecting a bacterial cell that expresses mRNA encoding Pasteurella multocida heparin synthase, and in vitro sulfation of a heparin polymer (claimed). The methods and compositions of the present invention are useful for polymer grafting and the production of non-naturally occurring chimeric polymers incorporating stretches of one or more acidic GAG molecules, such as heparin, chondroitin, hyaluronan and/or heparosan.

Dwg.0/4

L36 ANSWER 3 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2002-049237 [06] WPIDS

DOC. NO. CPI: C2002-013799

TITLE: New chondroitin synthase gene obtained from Pasteurella multocida, useful as hyaluronan polysaccharide substitute in medial or cosmetic applications, e.g. for eye or joint applications, for moisturizer or wound dressings.

DERWENT CLASS: B04 D16

INVENTOR(S): WEIGEL, J A; WEIGEL, P H; ZHOU, B; DE ANGELIS, P L; DEANGELIS, P L; JING, W

PATENT ASSIGNEE(S): (UYOK-N) UNIV OKLAHOMA; (DANG-I) DE ANGELIS P L; (DEAN-I) DEANGELIS P L; (JING-I) JING W

COUNTRY COUNT: 96

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001080810	A2	20011101	(200206)*	EN	125
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001053805	A	20011107	(200219)		
EP 1278830	A2	20030129	(200310)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
EP 1282684	A2	20030212	(200312)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
US 2003104601	A1	20030605	(200339)		
JP 2004512013	W	20040422	(200428)		295
US 2004132143	A1	20040708	(200445)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001080810	A2	WO 2001-US13395	20010425
AU 2001053805	A	AU 2001-53805	20010425
EP 1278830	A2	EP 2001-928880	20010425
		WO 2001-US13403	20010425

EP 1282684	A2		EP 2001-927344	20010425
			WO 2001-US13395	20010425
US 2003104601	A1	CIP of	US 1999-283402	19990401
		CIP of	US 1999-437277	19991110
		Provisional	US 2000-199538P	20000425
			US 2001-842484	20010425
JP 2004512013	W		JP 2001-577911	20010425
			WO 2001-US13395	20010425
US 2004132143	A1	Provisional	US 1998-80414P	19980402
		Provisional	US 1998-107929P	19981111
		CIP of	US 1999-283402	19990401
		CIP of	US 1999-437277	19991110
		Provisional	US 2000-199538P	20000425
		CIP of	US 2001-842484	20010425
		Provisional	US 2001-289554P	20010508
		CIP of	US 2002-142143	20020508
		CIP of	US 2002-195908	20020715
		Provisional	US 2002-404356P	20020816
		Provisional	US 2003-479432P	20030618
			US 2003-642248	20030815

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001053805	A	Based on	WO 2001080810
EP 1278830	A2	Based on	WO 2001081544
EP 1282684	A2	Based on	WO 2001080810
US 2003104601	A1	CIP of	US 6444447
JP 2004512013	W	Based on	WO 2001080810
US 2004132143	A1	CIP of	US 6444447

PRIORITY APPLN. INFO: US 2000-199538P 20000425; US 2000-245320P 20001102; US 1999-283402 19990401; US 1999-437277 19991110; US 2001-842484 20010425; US 1998-80414P 19980402; US 1998-107929P 19981111; US 2001-289554P 20010508; US 2002-142143 20020508; US 2002-195908 20020715; US 2002-404356P 20020816; US 2003-479432P 20030618; US 2003-642248 20030815

AN 2002-049237 [06] WPIDS

AB WO 200180810 A UPAB: 20020128

NOVELTY - A purified nucleic acid (I) comprising a coding region encoding enzymatically active chondroitin synthase, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) purified nucleic acid segments having a coding region encoding enzymatically active chondroitin synthase, where the nucleic acid segment is capable of hybridizing to a fully defined sequence of 2941 (S1) base pairs, as given in the specification, with (semi)conservative amino acid changes, or is a truncated segment;

(2) a recombinant vector selected from a plasmid, cosmid, phage, integrated cassette or virus vector, and comprises (I);

(3) recombinant host cells **transformed** with a recombinant vector comprising (I) or a nucleic acid encoding chondroitin synthase, or which contains a chondroitin synthase and an epimerase and/or sulfotransferase;

(4) purified compositions comprising an enzymatically active chondroitin synthase polypeptide, or a chondroitin polymer;

(5) producing a chondroitin polymer in vitro or in vivo;

(6) detecting a DNA species, comprising obtaining a DNA sample, contacting the sample with S1 or S2, hybridizing the DNA and (S1) to form a hybridized complex, and detecting the complex;

(7) detecting a cell or a bacterial cell that expresses mRNA encoding Pasteurella multocida chondroitin synthase;

(8) pharmaceutical composition comprising a pre-selected pharmaceutical drug and a chondroitin polymer produced by a chondroitin synthase directly or after modification of the polymer by sulfation and/or epimerization;

(9) an isolated nucleic acid segment encoding chondroitin synthase having a nucleic acid segment sufficiently duplicative of (S1) segment to allow possession of the biological property of encoding a Pasteurella multocida chondroitin synthase;

(10) a recombinant host that produce chondroitin synthase;

(11) a recombinant method of producing a **heterologous** polypeptide in a host cell;

(12) producing a chondroitin polymer by fermentation of a cell expressing a chondroitin synthase having a defined sequence of 961 amino acids;

(13) in vitro sulfation of a chondroitin polymer;

(14) a dermatan polymer obtained by epimerizing a chondroitin polymer;

(15) a recombinantly produced unsulfated chondroitin polysaccharide;

(16) a polysaccharide comprising alternating Beta 1,4-linked GalNAc and Beta 1,3-linked BlcUA in a 1:1 ratio of the polysaccharide;

(17) a nucleic acid segment corresponding to residues 1-704, 45-704, or 75-704 of (S1) and which encodes an enzymatically active chondroitin synthase; and

(18) a purified composition comprising a chondroitin synthase polypeptide, a chondroitin polymer.

USE - Chondroitin polysaccharide may be used as hyaluronan polysaccharide substitute in medial or cosmetic applications, e.g. for eye or joint applications, for moisturizer or wound dressings. The enzyme may be used in covalently coupling specific drugs, protein or toxins to the structurally modified chondroitin for general or targeted drug delivery or radiological procedures; covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other tree dimensional biomaterial with stronger physical properties, and covalently linking hyaluronic acid to a surface to create a biocompatible film or monolayer.

Dwg.0/10

L36 ANSWER 4 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2001-266071 [27] WPIDS
CROSS REFERENCE: 2003-635185 [60]
DOC. NO. NON-CPI: N2001-190255
DOC. NO. CPI: C2001-080571
TITLE: Removing target nucleic acid sequences e.g. selectable marker genes, genes involved in plant cell metabolism, growth development and fertility from plastid genomes, by Cre-mediated site specific recombination.
DERWENT CLASS: C06 D16 P13
INVENTOR(S): CORNEILLE, S; LUTZ, K; MALIGA, P
PATENT ASSIGNEE(S): (RUTF) UNIV RUTGERS STATE NEW JERSEY
COUNTRY COUNT: 95
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001021768	A1	20010329	(200127)*	EN	83

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM
DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC
LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE
SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001040176 A 20010424 (200141)
EP 1218488 A1 20020703 (200251) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
RO SE SI

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001021768	A1	WO 2000-US25930	20000921
AU 2001040176	A	AU 2001-40176	20000921
EP 1218488	A1	EP 2000-963696	20000921
		WO 2000-US25930	20000921

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001040176	A	Based on	WO 2001021768
EP 1218488	A1	Based on	WO 2001021768

PRIORITY APPLN. INFO: US 2000-211139P 20000613; US
1999-155007P 19990921

AN 2001-266071 [27] WPIDS
CR 2003-635185 [60]
AB WO 200121768 A UPAB: 20030919
NOVELTY - Selecting plant cells (C) expressing proteins encoded by a DNA **construct** having a nucleic acid (NA) encoding a marker, excision sites (ES) and plastid targeting sequence for homologous recombination into plastid genome at target sequence (T), comprising introducing a **construct** having NA encoding protein with excision activity into a selected (C), whose expression acts on ES excising (T).

DETAILED DESCRIPTION - Site specific recombination (I) for removal of predetermined NA sequences from the plastid genome, comprises:

(a) providing a first NA **construct**, comprising a promoter operably linked to a NA encoding an optional plastid targeting transit sequence which is operably linked to a NA encoding a protein having excision activity and further comprising a selectable marker encoding NA having plant specific 5' and 3' regulatory NA sequences;

(b) providing a second DNA **construct**, comprising a second selectable marker encoding NA and ES, optionally containing a gene of interest and further comprising **flanking** plastid targeting NA sequences which facilitate homologous recombination into plastid genome at a predetermined (T) such that ES **flank** the predetermined (T) following **homologous** recombination;

(c) introducing the second DNA **construct** into (C);

(d) culturing (C) in the presence of a selection agent, to select for those (C) expressing the proteins encoded by the second DNA **construct**; and

(e) introducing the first DNA **construct** into the selected (C) in the presence of a selection agent and selecting those (C) expressing proteins encoded by the first **construct** which when present acts on ES, excising the predetermined (T).

INDEPENDENT CLAIMS are also included for the following:

(1) a plant (II) regenerated from (I);

(2) a site specific recombination system comprising constructs of

(I); and
(3) progeny plants obtained from (II).
USE - The method is useful for removing **heterologous** sequences from the plastid genome, such as selectable marker genes following successful isolation of **transformed** progeny and to remove endogenous genes associated with male sterility, clpP ribosomal proteins and ribosomal RNA operon sequences from the plastid genome (claimed).
Dwg.0/20

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

```
L1            0 INITIAT? (W) DNA (W) UPTAKE
L2          373 INITIAT? (S) DNA (S) UPTAKE
L3         4746 NON (W) HOMOLOGOUS
L4            0 L2 AND L3
L5          209 STUFFER AND DNA
L6            0 L5 AND L2
L7         2254 DNA (W) UPTAKE
L8            1 L7 AND L3
L9            0 L5 AND L7
L10       18629 DNA (S) UPTAKE
L11           0 L10 AND L5
L12           7 L10 AND L3
L13           4 DUP REM L12 (3 DUPLICATES REMOVED)
                E DIAZ (W) TORRES MARIA/AU
                E DIAZ TORRES MARIA/AU
L14          54 E1-E4
L15          23 DUP REM L14 (31 DUPLICATES REMOVED)
L16           2 TRANSFORM? AND L15
L17           0 L3 AND L5
L18     1447160 TRANSFORM?
L19         470 L3 AND L18
L20           0 L19 AND L5
L21           5 L19 AND L10
L22           2 DUP REM L21 (3 DUPLICATES REMOVED)
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FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:39:56 ON 11 MAR 2005

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L23          33 CONSTRUCT AND L19
L24          19 DUP REM L23 (14 DUPLICATES REMOVED)
L25          63 FLANK? AND L19
L26          27 DUP REM L25 (36 DUPLICATES REMOVED)
L27           6 L24 AND L26
L28          21 L26 NOT L27
L29      133659 HETEROLOGOUS
L30       14048 L29 AND L18
L31        1925 (CONSTRUCT OR FLANK?) AND L30
L32           3 L5 AND L31
L33           3 DUP REM L32 (0 DUPLICATES REMOVED)
L34          63 HOMOLOGOUS (5N) (FLANK OR STUFFER)
L35           4 L31 AND L34
L36           4 DUP REM L35 (0 DUPLICATES REMOVED)
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=> homologous and l31

L37 380 HOMOLOGOUS AND L31

=> d scan l37

L37 380 ANSWERS BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Structural organization and genomic sequence of mouse syndecan-1 gene.
IT Sequence Data
Z22532: Genbank
IT Miscellaneous Descriptors
DNA EFFECTOR RESPONSE; DNA-DEPENDENT ATPASE ACTIVITY; NUCLEOTIDE SPECIFICITY; PREINITIATION COMPLEX; PROTEIN KINASE ACTIVITY

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):2

L37 380 ANSWERS CAPLUS COPYRIGHT 2005 ACS on STN
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 10
TI **Heterologous** modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe
ST Schizosaccharomyces gene targeting PCR deletion tagging; fission yeast gene targeting deletion tagging
IT Mutation
(deletion, gene deletion; **heterologous** modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe)
IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gene nmt1; **heterologous** modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe)
IT Gene targeting
PCR (polymerase chain reaction)
Schizosaccharomyces pombe
Transformation, genetic
(**heterologous** modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe)
IT Recombination, genetic
(integration, **homologous**; **heterologous** modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe)
IT Genetic markers
(kanMX6; **heterologous** modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe)
IT Plasmids
(templates; **heterologous** modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe)

L37 380 ANSWERS CAPLUS COPYRIGHT 2005 ACS on STN
CC 10-2 (Microbial Biochemistry)
Section cross-reference(s): 36
TI The yeast acid phosphatase can enter the secretory pathway without its N-terminal signal sequence
ST Saccharomyces acid phosphatase transport; signal peptide acid phosphatase yeast
IT Saccharomyces cerevisiae
(acid phosphatase transport by, signal sequence in relation to)
IT Protein sequences
(of acid phosphatase, of Saccharomyces cerevisiae)
IT Deoxyribonucleic acid sequences
(acid phosphatase-specifying, of Saccharomyces cerevisiae)
IT Mutation
(deletion, in acid phosphatase gene, of Saccharomyces cerevisiae)
IT Biological transport

(secretion, of acid phosphatase, by Saccharomyces cerevisiae, signal sequence in relation to)
IT Peptides, biological studies
RL: BIOL (Biological study)
(signal, of acid phosphatase, of Saccharomyces cerevisiae, protein secretion and glycosidation in relation to)
IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(PHO5, for acid phosphatase, of Saccharomyces cerevisiae, deletion mutation in)
IT 9001-77-8, Acid phosphatase
RL: PROC (Process)
(transport of, by Saccharomyces cerevisiae, signal sequence in relation to)

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):end

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

L1	0	INITIAT? (W) DNA (W) UPTAKE
L2	373	INITIAT? (S) DNA (S) UPTAKE
L3	4746	NON (W) HOMOLOGOUS
L4	0	L2 AND L3
L5	209	STUFFER AND DNA
L6	0	L5 AND L2
L7	2254	DNA (W) UPTAKE
L8	1	L7 AND L3
L9	0	L5 AND L7
L10	18629	DNA (S) UPTAKE
L11	0	L10 AND L5
L12	7	L10 AND L3
L13	4	DUP REM L12 (3 DUPLICATES REMOVED) E DIAZ (W) TORRES MARIA/AU E DIAZ TORRES MARIA/AU
L14	54	E1-E4
L15	23	DUP REM L14 (31 DUPLICATES REMOVED)
L16	2	TRANSFORM? AND L15
L17	0	L3 AND L5
L18	1447160	TRANSFORM?
L19	470	L3 AND L18
L20	0	L19 AND L5
L21	5	L19 AND L10
L22	2	DUP REM L21 (3 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:39:56 ON 11 MAR 2005

L23	33	CONSTRUCT AND L19
L24	19	DUP REM L23 (14 DUPLICATES REMOVED)
L25	63	FLANK? AND L19
L26	27	DUP REM L25 (36 DUPLICATES REMOVED)
L27	6	L24 AND L26
L28	21	L26 NOT L27
L29	133659	HETEROLOGOUS
L30	14048	L29 AND L18
L31	1925	(CONSTRUCT OR FLANK?) AND L30
L32	3	L5 AND L31

```
L33           3 DUP REM L32 (0 DUPLICATES REMOVED)
L34          63 HOMOLOGOUS (5N) (FLANK OR STUFFER)
L35           4 L31 AND L34
L36           4 DUP REM L35 (0 DUPLICATES REMOVED)
L37         380 HOMOLOGOUS AND L31

=> dup rem l34
PROCESSING COMPLETED FOR L34
L38          29 DUP REM L34 (34 DUPLICATES REMOVED)

=> t ti l38 1-29

L38  ANSWER 1 OF 29  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   Preparation of eukaryotic cells negative for dihydrofolate reductase,
     useful, after transformation, for optimized production of selected
     proteins, by homologous recombination.

L38  ANSWER 2 OF 29  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Segmental duplications flank the multiple sclerosis locus on chromosome
     17q

L38  ANSWER 3 OF 29  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Construction of a fowlpox virus transfer vector and its identification

L38  ANSWER 4 OF 29  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   Preparing library of protein-producing eukaryotic cells, useful for
     producing humanized high-affinity antibodies, comprises introducing
     specific recombination signals into chromosomal gene loci and integrating
     a variety of DNA sequences.

L38  ANSWER 5 OF 29  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 1
TI   Food-grade expression of human Cu/Zn-superoxide dismutase gene in
     Lactococcus lactis.

L38  ANSWER 6 OF 29     MEDLINE on STN                    DUPLICATE 2
TI   Three-dimensional structure of collagen fibril of pigskin.

L38  ANSWER 7 OF 29  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   New purified nucleic acid segment, useful for polymer grafting and the
     production of non-naturally occurring chimeric polymers, comprises a
     region encoding enzymatically active heparin synthase.

L38  ANSWER 8 OF 29  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   Novel nucleotide construct for generating DNA constructs for introducing
     into embryonic stem cell, comprising a sequence encoding a positive
     selection marker flanked by restriction enzyme sites.

L38  ANSWER 9 OF 29  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   A nucleotide construct contains a positive selection marker flanked by
     restriction sites and sequences that can be treated to produce single
     stranded regions and is useful for introducing targeted mutations into
     embryonic stem cells.

L38  ANSWER 10 OF 29  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   Novel nucleotide construct useful for disrupting function of gene in
     embryonic stem cell, comprises sequence encoding positive selection marker
     flanked by restriction enzyme sites, to create a single-stranded region.

L38  ANSWER 11 OF 29  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   Screening DNA library for selected gene, useful e.g. for creating knockout
     animals, based on homologous recombination with sequence that includes a
```

positive selection marker.

L38 ANSWER 12 OF 29 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
TI Entire sequence of a mouse chromosomal segment containing the gene Rhced and a comparative analysis of the homologous human sequence.

L38 ANSWER 13 OF 29 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
TI Novel vectors and system for selectable targeted integration of transgenes into a chromosome without antibiotic resistance markers

L38 ANSWER 14 OF 29 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI New chondroitin synthase gene obtained from Pasteurella multocida, useful as hyaluronan polysaccharide substitute in medial or cosmetic applications, e.g. for eye or joint applications, for moisturizer or wound dressings.

L38 ANSWER 15 OF 29 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Removing target nucleic acid sequences e.g. selectable marker genes, genes involved in plant cell metabolism, growth development and fertility from plastid genomes, by Cre-mediated site specific recombination.

L38 ANSWER 16 OF 29 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Screening for interactions between human beta amyloid precursor protein and human lon-protease like protein, useful for treating neurodegenerative disease.

L38 ANSWER 17 OF 29 MEDLINE on STN DUPLICATE 4
TI Cleavage of symmetric immobile DNA junctions by Escherichia coli RuvC.

L38 ANSWER 18 OF 29 MEDLINE on STN DUPLICATE 5
TI Characterization of the glutathione S-transferase GSTT1 deletion: discrimination of all genotypes by polymerase chain reaction indicates a trimodular genotype-phenotype correlation.

L38 ANSWER 19 OF 29 MEDLINE on STN DUPLICATE 6
TI Conservation of ARS elements and chromosomal DNA replication origins on chromosomes III of Saccharomyces cerevisiae and S. carlsbergensis.

L38 ANSWER 20 OF 29 MEDLINE on STN DUPLICATE 7
TI Dystrobrevin and dystrophin: an interaction through coiled-coil motifs.

L38 ANSWER 21 OF 29 MEDLINE on STN DUPLICATE 8
TI PCR-based study of conserved and variable DNA sequences of Tritrichomonas foetus isolates from Saskatchewan, Canada.

L38 ANSWER 22 OF 29 MEDLINE on STN DUPLICATE 9
TI DNA sequences tightly bound to proteins in mouse chromatin: identification of murine MER sequences.

L38 ANSWER 23 OF 29 MEDLINE on STN DUPLICATE 10
TI Detection of molecular heterogeneity in GH-1 gene deletions by analysis of polymerase chain reaction amplification products.

L38 ANSWER 24 OF 29 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
TI The primary structures of the flavodoxins from two strains of Desulfovibrio gigas. Cloning and nucleotide sequence of the structural genes.

L38 ANSWER 25 OF 29 MEDLINE on STN DUPLICATE 11
TI Ac induces homologous recombination at the maize P locus.

L38 ANSWER 26 OF 29 MEDLINE on STN DUPLICATE 12
TI Pseudomonas aeruginosa plasmids as suicide vectors in Escherichia coli: resolution of genomic cointegrates through short regions of homology.

L38 ANSWER 27 OF 29 MEDLINE on STN DUPLICATE 13
TI Immunoglobulin variable region heptamer-nonamer recognition sequence joined to rearranged D-J segment: implications for the immunoglobulin recombinase mechanism.

L38 ANSWER 28 OF 29 MEDLINE on STN DUPLICATE 14
TI The primary structures of two yeast enolase genes. Homology between the 5' noncoding flanking regions of yeast enolase and glyceraldehyde-3-phosphate dehydrogenase genes.

L38 ANSWER 29 OF 29 CAPLUS COPYRIGHT 2005 ACS on STN
TI On the use of plasmids for study of genetic transformation in Bacillus subtilis

=> l38 not l35
L39 25 L38 NOT L35

=> d ibib abs l39 1-25

L39 ANSWER 1 OF 25 MEDLINE on STN
ACCESSION NUMBER: 2003409209 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12947688
TITLE: Three-dimensional structure of collagen fibril of pigskin.
AUTHOR: Li Zhiqiang; Wang Yingme; Chen Min; Liao Longli; Xiang Tao; Guo Yang; Zhao Chunpeng; Yunfei Tian
CORPORATE SOURCE: Key Laboratory of Leather Chemistry and Engineering of Ministry of Education, Sichuan University, Chengdu 610065, China.
SOURCE: Sichuan da xue xue bao. Yi xue ban = Journal of Sichuan University. Medical science edition, (2003 Apr) 34 (2) 200-2.
Journal code: 101162609. ISSN: 1672-173X.
PUB. COUNTRY: China
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Chinese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200407
ENTRY DATE: Entered STN: 20030902
Last Updated on STN: 20040716
Entered Medline: 20040715

AB OBJECTIVE: To probe deply into the three-dimensional structure of pigskin collagen fibril and provide the basic data for using the pigskin tissue as tissue engineering material. METHODS: Scanning Probe Microscope (SPM) and Transmission Electron Microscope (TEM) were employed to study the three-dimensional structure of collagen fibril in pigskin tissue. RESULTS: Microscopy revealed that pigskin collagen fibril had periodic transverse groove (i.e. D-periodicity) which was about 67 nm. The diameter of fibril ranged from 57 to 135 nm, showing much difference among the papillary layer, reticular layer and infra-reticular layer. The length of fibril varied from 5 to 13 microns. Both ends of fibril were rotund and slightly bulgy. The fibrils assembled and the D-periodicities were **homologous** in **flank**. In axial direction fibrils were found staggered end by end. CONCLUSION: The data obtained in this study on the three-dimensional structure of pigskin collagen fibril are of significance to researches in tissue engineering materials.

L39 ANSWER 2 OF 25 MEDLINE on STN
ACCESSION NUMBER: 2001090847 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10975610
TITLE: Characterization of the glutathione S-transferase GSTT1 deletion: discrimination of all genotypes by polymerase chain reaction indicates a trimodular genotype-phenotype correlation.
AUTHOR: Sprenger R; Schlagenhaufer R; Kerb R; Bruhn C; Brockmoller J; Roots I; Brinkmann U
CORPORATE SOURCE: Epidauros Biotechnology, Pharmacogenetics Laboratory, Bernried, Germany.
SOURCE: Pharmacogenetics, (2000 Aug) 10 (6) 557-65.
Journal code: 9211735. ISSN: 0960-314X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010125

AB Glutathione S-transferase theta enzyme activity involved in the metabolism of toxic compounds is absent in approximately 20% of Caucasians due to a homozygous deletion of GSTT1 (*0/0). Because the exact manner of the GSTT1 deletion was unknown, current genotyping of GSTT1 was limited to detect the presence versus complete absence of the gene by a GSTT1-specific polymerase chain reaction (PCR). Thus, heterozygous (*A/0) and homozygous (*A/A) samples could not be discriminated. We have characterized the boundaries of the deletion of the human glutathione S-transferase theta (GSTT1) gene: PCR mapping and sequencing revealed a 54251 bp fragment including GSTT1 to be deleted from chromosome 22, most likely by a homologous recombination event between two highly **homologous** sequence stretches that **flank** GSTT1. Based on the knowledge of the GSTT1*0 region, a PCR assay was devised for unambiguous discrimination of homozygously deleted (*0/0), heterozygously (*A/0) and homozygously GSTT1 carrying (*A/A) individuals. Genotyping of 180 samples of a Caucasian population revealed that the deletion consists of one defined allele, whose distribution in the population fits the Hardy-Weinberg equilibrium with observed 20% *0/0, 46% *A/0 and 34% *A/A individuals. The number of GSTT1*A alleles detected by this procedure correlated highly significant with the enzyme activity in erythrocytes. Genotype-phenotype comparisons demonstrated a codominant type of inheritance by a gene-dose effect: samples with two active alleles expressed a statistically significant higher enzymatic activity compared to those with one null allele ($P < 0.0001$, ANOVA).

L39 ANSWER 3 OF 25 MEDLINE on STN
ACCESSION NUMBER: 2001013101 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11009612
TITLE: Cleavage of symmetric immobile DNA junctions by Escherichia coli RuvC.
AUTHOR: Sha R; Iwasaki H; Liu F; Shinagawa H; Seeman N C
CORPORATE SOURCE: Department of Chemistry, New York University, New York, New York 10003, USA.
CONTRACT NUMBER: GM-29554 (NIGMS)
SOURCE: Biochemistry, (2000 Oct 3) 39 (39) 11982-8.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010

ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20020917
Entered Medline: 20001027

AB The Holliday junction is a key DNA intermediate in the process of genetic recombination. It consists of two double-helical domains composed of **homologous** strands that **flank** a branch point; two of the strands are roughly helical, and two form the crossover between the helices. RuvC is a Holliday junction resolvase that cleaves the helical strands at a symmetric sequence, leading to the production of two recombinant molecules. We have determined the position of the cleavage site relative to the crossover point by the use of symmetric immobile junctions; these are DNA molecules containing two crossover points, one held immobile by sequence asymmetry and the second a symmetric sequence, but held immobile by torsional coupling to the first junction. We have built five symmetric immobile junctions, in which the tetranucleotide recognition site is moved stepwise relative to the branch point. We have used kinetic analysis of catalysis, gel retardation, and hydroxyl radical hypersensitivity to analyze this system. We conclude that the internucleotide linkage one position 3' to the crossover point is the favored site of cleavage.

L39 ANSWER 4 OF 25 MEDLINE on STN
ACCESSION NUMBER: 1999318829 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10388813
TITLE: Conservation of ARS elements and chromosomal DNA replication origins on chromosomes III of Saccharomyces cerevisiae and S. carlsbergensis.
AUTHOR: Yang C; Theis J F; Newlon C S
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, New Jersey Medical School and Graduate School of Biomedical Sciences, University of Medicine and Dentistry of New Jersey, Newark, New Jersey 07103, USA.
CONTRACT NUMBER: GM-35679 (NIGMS)
HG-00027 (NHGRI)
SOURCE: Genetics, (1999 Jul) 152 (3) 933-41.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19991005
Last Updated on STN: 20000303
Entered Medline: 19990923

AB DNA replication origins, specified by ARS elements in Saccharomyces cerevisiae, play an essential role in the stable transmission of chromosomes. Little is known about the evolution of ARS elements. We have isolated and characterized ARS elements from a chromosome III recovered from an alloploid Carlsberg brewing yeast that has diverged from its S. cerevisiae homeologue. The positions of seven ARS elements identified in this S. carlsbergensis chromosome are conserved: they are located in intergenic regions flanked by open reading frames **homologous** to those that **flank** seven ARS elements of the S. cerevisiae chromosome. The S. carlsbergensis ARS elements were active both in S. cerevisiae and S. monacensis, which has been proposed to be the source of the diverged genome present in brewing yeast. Moreover, their function as chromosomal replication origins correlated strongly with the activity of S. cerevisiae ARS elements, demonstrating the conservation of ARS activity and replication origin function in these two species.

L39 ANSWER 5 OF 25 MEDLINE on STN
ACCESSION NUMBER: 1998024145 MEDLINE

DOCUMENT NUMBER: PubMed ID: 9356463
TITLE: Dystrobrevin and dystrophin: an interaction through coiled-coil motifs.
AUTHOR: Sadoulet-Puccio H M; Rajala M; Kunkel L M
CORPORATE SOURCE: Department of Genetics, Harvard Medical School, Boston, MA 02115, USA.
CONTRACT NUMBER: NS23740 (NINDS)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1997 Nov 11) 94 (23) 12413-8.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109
Entered Medline: 19971216

AB Dystrobrevin, a dystrophin-related and -associated protein, has been proposed to be important in the formation and maintenance of the neuromuscular junction. Dystrobrevin coprecipitates with both the acetylcholine receptor complex as well as the dystrophin glycoprotein complex. Although the nature of dystrobrevin's association with the dystrophin glycoprotein complex remains unclear, it is known that dystrobrevin binds directly to the syntrophins, a heterologous group of dystrophin-associated proteins. Using the yeast two-hybrid system to identify protein-protein interactions, we present evidence for the heterodimerization of dystrobrevin directly with dystrophin. The C terminus of dystrobrevin binds specifically to the C terminus of dystrophin. We further refined this site of interaction to these proteins' **homologous** coiled-coil motifs that **flank** their respective syntrophin-binding sites. We also show that the interaction between the dystrobrevin and dystrophin coiled-coil domains is specific and is not due to a nonspecific coiled-coil domain interaction. From the accumulated evidence of protein-protein interactions presented here and elsewhere, we propose a partially revised model of the organization of the dystrophin-associated glycoprotein complex.

L39 ANSWER 6 OF 25 MEDLINE on STN
ACCESSION NUMBER: 95340767 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7615746
TITLE: PCR-based study of conserved and variable DNA sequences of Tritrichomonas foetus isolates from Saskatchewan, Canada.
AUTHOR: Riley D E; Wagner B; Polley L; Krieger J N
CORPORATE SOURCE: Department of Urology, University of Washington School of Medicine, Seattle 98195, USA.
CONTRACT NUMBER: RO1 DK38955 (NIDDK)
SOURCE: Journal of clinical microbiology, (1995 May) 33 (5) 1308-13.
Journal code: 7505564. ISSN: 0095-1137.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199508
ENTRY DATE: Entered STN: 19950905
Last Updated on STN: 19950905
Entered Medline: 19950818

AB The protozoan parasite Tritrichomonas foetus causes infertility and spontaneous abortion in cattle. In Saskatchewan, Canada, the culture prevalence of trichomonads was 65 of 1,048 (6%) among 1,048 bulls tested within a 1-year period ending in April 1994. Saskatchewan was previously

thought to be free of the parasite. To confirm the culture results, possible T. foetus DNA presence was determined by the PCR. All of the 16 culture-positive isolates tested were PCR positive by a single-band test, but one PCR product was weak. DNA fingerprinting by both T17 PCR and randomly amplified polymorphic DNA PCR revealed genetic variation or polymorphism among the T. foetus isolates. T17 PCR also revealed conserved loci that distinguished these T. foetus isolates from Trichomonas vaginalis, from a variety of other protozoa, and from prokaryotes. TCO-1 PCR, a PCR test designed to sample DNA sequence **homologous** to the 5' **flank** of a highly conserved cell division control gene, detected genetic polymorphism at low stringency and a conserved, single locus at higher stringency. These findings suggested that T. foetus isolates exhibit both conserved genetic loci and polymorphic loci detectable by independent PCR methods. Both conserved and polymorphic genetic loci may prove useful for improved clinical diagnosis of T. foetus. The polymorphic loci detected by PCR suggested either a long history of infection or multiple lines of T. foetus infection in Saskatchewan. Polymorphic loci detected by PCR may provide data for epidemiologic studies of T. foetus.

L39 ANSWER 7 OF 25 MEDLINE on STN
ACCESSION NUMBER: 94296557 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8024697
TITLE: DNA sequences tightly bound to proteins in mouse chromatin: identification of murine MER sequences.
AUTHOR: Avramova Z; Georgiev O; Tsanev R
CORPORATE SOURCE: Institute of Molecular Biology, Bulgarian Academy of Sciences, Sofia.
SOURCE: DNA and cell biology, (1994 May) 13 (5) 539-48. Journal code: 9004522. ISSN: 1044-5498.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L36330; GENBANK-L36331; GENBANK-L36332; GENBANK-L36333; GENBANK-L36334; GENBANK-L36335; GENBANK-L36336; GENBANK-L36337
ENTRY MONTH: 199408
ENTRY DATE: Entered STN: 19940818
Last Updated on STN: 19970203
Entered Medline: 19940809

AB The finding of stably (tightly) associated DNA-protein complexes in eukaryotic chromatin has provoked many hypotheses and speculations concerning their possible role. While the answer of this question is not envisaged yet, it is clear that elucidation of the nature of the individual components involved in such complexes is a necessary step in this direction. Here, the nature of several mouse DNA sequences in the vicinity of a putative stably attached protein is studied. Eight independently isolated clones containing such sequences were compared to known sequences in GenBank. Two clones were found to belong to different subfamilies of repetitive sequences, organized into a larger family--the L1md family. One clone harbors a sequence that is a member of the Alu-type family. Four of the cloned sequences are preset in low copy numbers, but the computer search found similar sequences in various genomic regions of different rodents. These facts, together with the finding that regions **homologous** to the above clones often **flank** other repetitive elements in the genome, suggest that the cloned sequences belong to new, not yet described families of repeats in the murine genome. It is possible that they correspond to the medium reiteration frequency sequences, MER-sequences, discovered recently in the human genome (Jurka, 1990; Kaplan and Duncan, 1990). Particularly intriguing is the homology found at the integration sites of polyoma virus

in two transformed cell lines with two of these clones.

L39 ANSWER 8 OF 25 MEDLINE on STN
ACCESSION NUMBER: 92193445 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1548341
TITLE: Detection of molecular heterogeneity in GH-1 gene deletions by analysis of polymerase chain reaction amplification products.
AUTHOR: Kamijo T; Phillips J A 3rd
CORPORATE SOURCE: Department of Pediatrics, Vanderbilt University School of Medicine, Nashville, Tennessee 37232.
CONTRACT NUMBER: DK-35592 (NIDDK)
RR-00095 (NCRR)
SOURCE: Journal of clinical endocrinology and metabolism, (1992 Apr) 74 (4) 786-9.
Journal code: 0375362. ISSN: 0021-972X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199204
ENTRY DATE: Entered STN: 19920509
Last Updated on STN: 19920509
Entered Medline: 19920422

AB At least three different sizes of GH-1 gene deletions (approximately 6.7, 7.0 and 7.6 kilobases) have been detected by Southern blot analysis of DNA from individuals with familial isolated GH deficiency type IA (IGHD1A). It is likely that these deletions result from unequal crossing over events between **homologous** regions that **flank** the GH-1 gene. Heterogeneity in clinical phenotypes is suggested by reports of good responses to exogenous GH treatment in most IGHD1A subjects with 7.6 kilobase deletions as opposed to poor responses in many subjects with smaller deletions. To determine if characteristic differences in gene deletions could be detected that correlate with response to treatment we analyzed the DNA sequences that normally flank the GH-1 gene. Digestion patterns of the PCR amplification products of these sequences from DNA of IGHD type IA patients with the restriction endonucleases BglI, HaeII, or SmaI showed characteristic differences for each of the three deletion sizes studied. The location and size of all deletions agreed with previous size estimates based on Southern blot analysis. Interestingly, clinical differences observed in the development of high titers of anti-GH antibodies and poor growth responses after GH treatment are unexplained, since discordant outcomes were observed in patients who had deletions of the same size and approximate location.

L39 ANSWER 9 OF 25 MEDLINE on STN
ACCESSION NUMBER: 92104491 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1761220
TITLE: Pseudomonas aeruginosa plasmids as suicide vectors in Escherichia coli: resolution of genomic cointegrates through short regions of homology.
AUTHOR: Dunn I S
CORPORATE SOURCE: Department of Pathology, University of Queensland, Medical School, Herston, Australia.
SOURCE: Gene, (1991 Dec 1) 108 (1) 109-14.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199202
ENTRY DATE: Entered STN: 19920302

Last Updated on STN: 19920302
Entered Medline: 19920213

AB Pseudomonas aeruginosa plasmids which cannot replicate in Escherichia coli have been used to introduce specific modifications into the E. coli chromosome by homologous recombination ('gene targeting'). The E. coli gene (gpt) encoding guanine-xanthine phosphoribosyltransferase (Gpt) was used for initial targeting studies owing to the availability of a powerful positive selection for loss of the Gpt+ phenotype (6-thioguanine resistance or 6TGR or Gpt-). P. aeruginosa plasmids containing selectable markers flanked by gpt sequences were introduced as supercoiled DNA into an E. coli strain which contained a normal gpt locus. Primary cointegration of such plasmids into the E. coli genome results in a gene duplication event which maintains Gpt function; a secondary recombinational event which resolves the cointegrate either reverses the primary event or results in replacement of the original gpt copy with the modified version. A 316-bp region of homology was sufficient for cointegrate formation, and resolution of the cointegrates through a shorter (92 bp) **homologous flank** was selectable through loss of Gpt function. The frequency of cointegrate resolution under these conditions was significantly above the spontaneous gpt mutational loss rate.

L39 ANSWER 10 OF 25 MEDLINE on STN
ACCESSION NUMBER: 91285393 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1648001
TITLE: Ac induces homologous recombination at the maize P locus.
AUTHOR: Athma P; Peterson T
CORPORATE SOURCE: Cold Spring Harbor Laboratory, New York 11724.
CONTRACT NUMBER: RO1 GM39832 (NIGMS)
SOURCE: Genetics, (1991 May) 128 (1) 163-73.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199108
ENTRY DATE: Entered STN: 19910825
Last Updated on STN: 19990129
Entered Medline: 19910805

AB The maize P gene conditions red phlobaphene pigmentation to the pericarp and cob. Starting from two unstable P alleles which carry insertions of the transposable element Ac, we have derived 51 P null alleles; 47 of the 51 null alleles have a 17-kb deletion which removes the 4.5-kb Ac element and 12.5 kb of P sequences flanking both sides of Ac. The deletion endpoints lie within two 5.2-kb **homologous** direct repeats which **flank** the P gene. A P allele which contains the direct repeats, but does not have an Ac insertion between the direct repeats, shows very little sporophytic or gametophytic instability. The apparent frequency of sporophytic mutations was not increased when Ac was introduced in trans. Southern analysis of DNA prepared from the pericarp tissue demonstrates that the deletions can occur premeiotically, in the somatic cells during development of the pericarp. Evidence is presented that the deletions occurred by homologous recombination between the two direct repeats, and that the presence of an Ac element at the P locus is associated with the recombination/deletion. These results add another aspect to the spectrum of activities of Ac: the destabilization of flanking direct repeat sequences.

L39 ANSWER 11 OF 25 MEDLINE on STN
ACCESSION NUMBER: 87196438 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3106497
TITLE: Immunoglobulin variable region heptamer-nonamer recognition

sequence joined to rearranged D-J segment: implications for the immunoglobulin recombinase mechanism.
AUTHOR: Stenzel-Poore M P; Rittenberg M B
CONTRACT NUMBER: AI 14985 (NIAID)
I U41 RR-01685-03 (NCRR)
SOURCE: Journal of immunology (Baltimore, Md. : 1950), (1987 May 1) 138 (9) 3055-9.
Journal code: 2985117R. ISSN: 0022-1767.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
OTHER SOURCE: GENBANK-M15993; GENBANK-M15994
ENTRY MONTH: 198705
ENTRY DATE: Entered STN: 19900303
Last Updated on STN: 19970203
Entered Medline: 19870529

AB We have found a novel immunoglobulin gene rearrangement in a murine hybridoma in which a heavy chain variable region (VH) heptamer-nonamer recognition sequence is joined to the diversity segment (D) through head-to-head fusion. The heptamer-nonamer recognition sequence and its adjacent 5' DNA are derived from the downstream flanking region of a germline VH gene. Sequence analysis indicates that this adjacent DNA is **homologous** to the downstream **flank** of VH108B, and it has characteristics of RNA processing that may suggest it was derived from an mRNA intermediate; these unusual features indicate that the segment is a processed gene. Because of head-to-head fusion, the recognition sequence and the flanking sequence are in opposite transcriptional polarity to D. The latter is joined correctly at its 3' border to a joining (J) gene segment. A gamma 1 constant region (but not mu) is located further downstream. Thus this fragment has several features common to normal immunoglobulin heavy chain gene rearrangement despite the unusual joining event involving V-D. Linkage of the VH heptamer-nonamer recognition sequence to D has not been observed previously. Although the recognition sequence described is inverted with respect to D and J, the endonucleolytic process that cleaved the recognition sequence at the 5' border of the heptamer before rearranging it to D was accurate. We suggest that of the three functions associated with the recombinase reaction; recognition, cutting, and ligation, only recognition and cutting may be limited to specific structures, and the ligation step may be less restricted because it is not confined to forming coding-to-coding or flank-to-flank joints. This aberrant ligation product suggests that the information leading to normal rearrangements may be found in structures that include more than the recognition sequences or coding regions alone, because the joining described here has spliced the incorrect end of a recognition sequence to a coding region to yield a nonproductive recombination.

L39 ANSWER 12 OF 25 MEDLINE on STN
ACCESSION NUMBER: 81094138 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6256394
TITLE: The primary structures of two yeast enolase genes. Homology between the 5' noncoding flanking regions of yeast enolase and glyceraldehyde-3-phosphate dehydrogenase genes.
AUTHOR: Holland M J; Holland J P; Thill G P; Jackson K A
SOURCE: Journal of biological chemistry, (1981 Feb 10) 256 (3) 1385-95.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-J01322; GENBANK-J01323; GENBANK-M10665
ENTRY MONTH: 198103
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19900316
Entered Medline: 19810327

AB Segments of yeast genomic DNA containing two enolase structural genes have been isolated by subculture cloning procedures using a cDNA hybridization probe synthesized from purified yeast enolase mRNA. Based on restriction endonuclease and transcriptional maps of these two segments of yeast DNA, each hybrid plasmid contains a region of extensive nucleotide sequence homology which forms hybrids with the cDNA probe. The DNA sequences which **flank** this **homologous** region in the two hybrid plasmids are nonhomologous indicating that these sequences are nontandemly repeated in the yeast genome. The complete nucleotide sequence of the coding as well as the flanking noncoding regions of these genes has been determined. The amino acid sequence predicted from one reading frame of both structural genes is extremely similar to that determined for yeast enolase (Chin, C. C. Q., Brewer, J. M., Eckard, E., and Wold, F. (1981) J. Biol. Chemical 256, 1370-1376), confirming that these isolated structural genes encode yeast enolase. The nucleotide sequences of the coding regions of the genes are approximately 95% homologous, and neither gene contains an intervening sequence. Codon utilization in the enolase genes follows the same biased pattern previously described for two yeast glyceraldehyde-3-phosphate dehydrogenase structural genes (Holland, J. P., and Holland, M. J. (1980) J. Biol. Chemical 255, 2596-2605). DNA blotting analysis confirmed that the isolated segments of yeast DNA are colinear with yeast genomic DNA and that there are two nontandemly repeated enolase genes per haploid yeast genome. The noncoding portions of the two enolase genes adjacent to the initiation and termination codons are approximately 70% homologous and contain sequences thought to be involved in the synthesis and processing messenger RNA. Finally there are regions of extensive homology between the two enolase structural genes and two yeast glyceraldehyde-3-phosphate dehydrogenase structural genes within the 5- noncoding portions of these glycolytic genes.

L39 ANSWER 13 OF 25 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:31509 BIOSIS
DOCUMENT NUMBER: PREV200400032955
TITLE: Food-grade expression of human Cu/Zn-superoxide dismutase gene in Lactococcus lactis.
AUTHOR(S): Wei Wenzhong; Xiang Hua; Tan Huarong [Reprint Author]
CORPORATE SOURCE: Institute of Microbiology, Chinese Academy of Sciences, Beijing, 100080, China
tanhr@sun.im.ac.cn
SOURCE: Weishengwu Xuebao, (June 2003) Vol. 43, No. 3, pp. 347-353. print.
CODEN: WSHPA8. ISSN: 0001-6209.
DOCUMENT TYPE: Article
LANGUAGE: Chinese
ENTRY DATE: Entered STN: 7 Jan 2004
Last Updated on STN: 7 Jan 2004

AB A food-grade gene expression system in L. lactis using the lacF gene as selection marker was constructed and further used for food-grade expression of human Cu/Zn superoxide dismutase (Cu/Zn SOD). Firstly, an integrative plasmid pUCEmDE containing **homologous** fragments with 0.5kb **flank** sequences of the lacF gene was constructed. The lacF gene was in-frame deleted by double cross-over between the plasmid pUCEmDE and the chromosomal DNA in L. lactis MG5267 and resulted in a food-grade host WZ103 that was confirmed by PCR and Lac phenotype examination. After that, a complementary plasmid pMG36eF in which the lacF gene was controlled by the strong constitutive promoter P32 was

electroporated into WZ103 and resulted in the restoration of Lac+ phenotype, indicating that the lacF function in WZ103 could be complemented by the lacF gene in pMG36eF. Finally, a food-grade plasmid pWZ104 used for the expression of Cu/Zn SOD was constructed, in which the lacF gene was used as a selective marker instead of any antibiotic resistance genes. Expressed Cu/Zn SOD in WZ103 (pWZ104) was demonstrated and showed biological activity through non-denatured PAGE and SOD activity gel-staining.

L39 ANSWER 14 OF 25 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1020937 CAPLUS
TITLE: Construction of a fowlpox virus transfer vector and its identification
AUTHOR(S): Zhi, Haidong; Wang, Yunfeng; Wang, Lili; Wang, Mei; Liu, Di; Tong, Guangzhi
CORPORATE SOURCE: Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Harbin, 150001, Peop. Rep. China
SOURCE: Zhongguo Shengwu Gongcheng Zazhi (2004), 24(7), 89-92
CODEN: ZSGZAW; ISSN: 1671-8135
PUBLISHER: Zhongguo Shengwu Gongcheng Zazhishe
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB Fowlpox virus has been used as safe vector to construct vaccines to control avian virus disease. Transfer vector construction is considered an important step in the construction of recombinant virus. Based on the sequence anal. of the genome of fowlpox virus, the ORF F11L was chosen as insertion site for the construction of transfer vector. The genomic DNA of Fowlpox was extracted, and the 1 kb **homologous flank** was amplified, then the segment was ligated in vitro and subcloned into pUC1149, therefore the transfer vector was named as pSY683. Based on the transfer vector pSY683, a transfer vector containing the LP2EP2 controlled EGFP was constructed, after transfection in chicken fibroblast cells infected with fowlpox virus, the reporter gene expressed 72 h later. This results lay the foundation for recombinant vaccine development.

L39 ANSWER 15 OF 25 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:692930 CAPLUS
DOCUMENT NUMBER: 141:406516
TITLE: Segmental duplications flank the multiple sclerosis locus on chromosome 17q
AUTHOR(S): Chen, Daniel C.; Saarela, Janna; Clark, Royden A.; Miettinen, Timo; Chi, Anthony; Eichler, Evan E.; Peltonen, Leena; Palotie, Aarno
CORPORATE SOURCE: Department of Human Genetics, David Geffen School of Medicine at UCLA, University of California, Los Angeles, CA, 90095, USA
SOURCE: Genome Research (2004), 14(8), 1483-1492
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Large chromosomal rearrangements, duplications, and inversions are relatively common in mammalian genomes. Here we report interesting features of DNA strands flanking a Multiple Sclerosis (MS) susceptibility locus on Chromosome 17q24. During the positional cloning process of this 3-Mb locus, several markers showed a radiation hybrid clone retention rate above the average (1.8-fold), suggestive for the existence of duplicated sequences in this region. FISH studies demonstrated multiple signals with three of the tested regional BACs, and 24 BACs out of 187 showed evidence for duplication in shotgun sequence comparisons of the 17q22-q24 region. Specifically, the MS haplotype region proved to be flanked by palindromic

sequence stretches and by long segmental intrachromosomal duplications in which highly homologous DNA sequences (>96% identity) are present at both ends of the haplotype. Moreover, the 3-Mb DNA segment, flanked by the duplications, is inverted in the mouse genome when compared with the orientation in human and chimp. The segmental duplication architecture surrounding the MS locus raises the possibility that a nonallelic homologous recombination between duplications could affect the biol. activity of the regional genes, perhaps even contributing to the genetic background of MS.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 16 OF 25 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:101329 CAPLUS
DOCUMENT NUMBER: 134:173877
TITLE: Novel vectors and system for selectable targeted integration of transgenes into a chromosome without antibiotic resistance markers
INVENTOR(S): Rosenberg, Susan M.; Lombardo, Mary-Jane; Gumbiner-Russo, Laura
PATENT ASSIGNEE(S): Baylor College of Medicine, USA
SOURCE: PCT Int. Appl., 64 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001009351	A1	20010208	WO 2000-US21053	20000802

W: AU, CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.: US 1999-146752P P 19990802

AB The invention relates to vectors and a method for creating a transgenic cell by neg. selecting cells deficient in integration of a transgene. The method comprises introducing a linear vector into the cell wherein said vector contains a cassette consisting of a 5' flanking sequence, a polylinker site containing a nucleic acid sequence of interest, and a 3' flanking sequence wherein the 5' and 3' flanking sequences are homologous to a sequence in a chromosome in the cell where the nucleic acid sequence of interest is to be inserted. The next step is integration of said vector into the chromosome through recombination between the flanking sequences and the homologous DNA sequences wherein said **homologous** DNA sequences **flank** a conditional killing module in a chromosome. The last step comprises the neg. selection against cells retaining said conditional killing module and deficient for integration of said linear vector. The TGV (TransGenic Escherichia coli Vectors) system for chromosomal gene expression is described. In a preferred embodiments said conditional killing module is λ xis1 cIts857 prophage or defective prophages λ cIts857 Δ(cro-bioA), λ cIts857 cIind- Δ(cro-bioA), λ xis1 cIts857 Δ(cro-bioA), λ cIts857 cIind- Δ(cro-attR), λ cIts857 cIind- P-BAD Δ(cro-attR).

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 17 OF 25 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1980:491744 CAPLUS
DOCUMENT NUMBER: 93:91744
TITLE: On the use of plasmids for study of genetic

transformation in Bacillus subtilis
AUTHOR(S): Dubnau, D.; Contente, S.; Gryczan, T. J.
CORPORATE SOURCE: Public Health Res. Inst., City New York, Inc., New York, NY, 10016, USA
SOURCE: Proceedings of the FEBS Meeting (1980), 63(DNA - Recomb., Interact. Repair), 365-86
CODEN: FEBPBY; ISSN: 0071-4402
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The transformation of B. subtilis competent cultures by plasmid DNA is a recE-independent 1st order process which requires multimeric CCC DNA. A model of plasmid transformation is presented which accounts for these properties. Transformation of recipients carrying a homologous resident plasmid by linear plasmid DNA, on the other hand, can occur by a process which is recE-dependent and which requires that **homologous** sequences **flank** the selected donor marker. Transformation by linear plasmids probably occurs by recombination and, thus, is a valid model for the study of bacterial transformation. A system for the cloning of foreign DNA in B. subtilis is developed.

L39 ANSWER 18 OF 25 EMBASE
on STN
ACCESSION NUMBER: 2002429610 EMBASE
TITLE: Entire sequence of a mouse chromosomal segment containing the gene Rhced and a comparative analysis of the homologous human sequence.
AUTHOR: Kumada M.; Iwamoto S.; Kamesaki T.; Okuda H.; Kajii E.
CORPORATE SOURCE: M. Kumada, Department of Legal Medicine, Jichi Medical School, Minamikawachi-machi, Kawachi-gun, Tochigi-ken 329-0498, Japan. kuman@jichi.ac.jp
SOURCE: Gene, (16 Oct 2002) 299/1-2 (165-172).
Refs: 32
ISSN: 0378-1119 CODEN: GENED6
PUBLISHER IDENT.: S 0378-1119(02)01054-5
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The mouse genomic sequence of the region containing the gene Rhced, the orthologue to the human gene RH30, was determined to elucidate the structure of Rhced and its flanking regions and to compare these with the corresponding human genomic region. Two genes, Smp1 and AK003528 (an orthologue of FLJ10747), **flank** Rhced. Neither sequences **homologous** to the characteristic nucleotide elements flanking the RHD gene in humans (rhesus boxes) nor an additional Rh gene were found within the mouse region sequenced. This result and that of a previous report demonstrate that this chromosomal region of the mouse comprises five genes (FLJ10747-RHCE-SMP1-NPD014-P29) that exhibit syntenic homology with the corresponding human region, which suggests that the RHD gene and rhesus boxes were inserted later. Evaluations of tissue distribution and subcellular localization of these genes indicate that the SMP1 orthologue has a ubiquitous tissue distribution and cytoplasmic localization, whereas AK003528 is expressed slightly higher in testis with a strong subcellular localization in the nucleus. Despite the steady improvements in the draft sequence of the human genome, this study demonstrates the continuing benefits of comparative genetic analyses in increasing our understanding of human genomic structure. .COPYRGT. 2002 Elsevier Science B.V. All rights reserved.

L39 ANSWER 19 OF 25 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 92231590 EMBASE
DOCUMENT NUMBER: 1992231590
TITLE: The primary structures of the flavodoxins from two strains of Desulfovibrio gigas. Cloning and nucleotide sequence of the structural genes.
AUTHOR: Helms L.R.; Swenson R.P.
CORPORATE SOURCE: Department of Biochemistry, Ohio State University, 484 West 12th Avenue,Columbus, OH 43210, United States
SOURCE: Biochimica et Biophysica Acta - Gene Structure and Expression, (1992) 1131/3 (325-328).
ISSN: 0167-4781 CODEN: BBGSD5
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The structural genes coding for the flavodoxin proteins from two different strains of the sulfate-reducing bacteria Desulfovibrio gigas (ATCC 19364/NCIB 9332 and ATCC 29494/DSM 496) have been identified, cloned and the nucleotide sequence established. The protein sequences derived from the gene from each strain share a sequence identity of 66% with regions directly involved in binding the flavin mononucleotide cofactor being the most **homologous**. Both aromatic residues that **flank** the flavin isoalloxazine ring in the crystal structure of the flavodoxin from D. vulgaris, i.e., Trp-60 and Tyr-98, are also present in these flavodoxin proteins. These observations stand in contrast to reports that the flavodoxin from Desulfovibrio gigas contains a single tryptophan residue which is located distant from the flavin binding site. Therefore, the FMN binding site of this flavodoxin is not distinct from the other Desulfovibrio flavodoxins in this regard.

L39 ANSWER 20 OF 25 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2004-051016 [05] WPIDS
CROSS REFERENCE: 2002-635678 [68]
DOC. NO. CPI: C2004-020470
TITLE: A nucleotide construct contains a positive selection marker flanked by restriction sites and sequences that can be treated to produce single stranded regions and is useful for introducing targeted mutations into embryonic stem cells.
DERWENT CLASS: B04 C06 D16
INVENTOR(S): BRENNAN, T J; KLEIN, R D
PATENT ASSIGNEE(S): (DELT-N) DELTAGEN INC
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2002197624	A1	20021226	(200405)*		37

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 2002197624	A1	Provisional	US 1997-84194P	19971117
		Provisional	US 1998-84949P	19980511
		Cont of	US 1998-193834	19981117
			US 2002-87523	20020228

PRIORITY APPLN. INFO: US 2002-87523 20020228; US
1997-84194P 19971117; US
1998-84949P 19980511; US
1998-193834 19981117

AN 2004-051016 [05] WPIDS

CR 2002-635678 [68]

AB US2002197624 A UPAB: 20040120

NOVELTY - A new nucleotide construct comprises a sequence encoding a positive selection marker flanked by restriction enzyme sites which are then flanked by sequences not complementary to each other and not including at least one base type at any position, where the construct can be treated so that single stranded regions are created at each sequence lacking at least one nucleotide.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(a) a construct having the 4768 nucleotide sequence fully defined in the specification (sequence I);

(b) a construct having the 6355 nucleotide sequence fully defined in the specification (sequence II);

(c) making a DNA construct useful in introducing a nucleotide sequence into a target DNA, comprising:

(a) amplifying in one reaction a first polynucleotide comprising two different nucleotide sequences substantially homologous to the target DNA; and

(b) inserting a second polynucleotide between the two different nucleotide sequences;

(d) making a DNA construct useful in introducing a nucleotide sequence into a target DNA, comprising:

(a) providing a polynucleotide substantially homologous to the target DNA;

(b) generating two different fragments of the polynucleotide;

(c) providing a vector having a gene encoding a positive selection marker; and

(d) using ligation independent cloning to insert the two different fragments into the vector to form the construct, where the positive selection marker is between the two different sequence fragments in the construct;

(e) a nucleotide construct comprising a sequence encoding a positive selection marker flanked on each side by at least one restriction enzyme site which itself is flanked by a pair of annealing sites which do not include at least one type of base at any position, where none of the annealing sites have complementary sequences and where the construct can be treated to create single stranded regions between the pair of annealing sites;

(f) a host cell containing the above construct;

(g) disrupting the function of a target sequence or gene in a cell, comprising:

(a) inserting sequences homologous to the target gene into the above construct so that the sequences **homologous** to the target **flank** the positive selection marker, to produce a targeting construct; and

(b) introducing the targeting construct into the cell to produce a homologous recombinant where the function of the target gene or sequence is disrupted;

(h) a targeting construct produced by the above method;

(i) a host cell containing the above targeting construct;

(j) an animal or plant containing the above targeting construct

USE - The invention is useful for introducing targeted mutations into embryonic stem cells.

DESCRIPTION OF DRAWING(S) - A schematic showing the pDG2 vector which contains an ampicillin resistance gene and a neomycin (Neo') gene. On each side of the Neo' gene are two sites for ligation independent cloning along with restriction sites.

Dwg.2/11

L39 ANSWER 21 OF 25 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-383833 [37] WPIDS
DOC. NO. CPI: C2003-102174
TITLE: Preparing library of protein-producing eukaryotic cells, useful for producing humanized high-affinity antibodies, comprises introducing specific recombination signals into chromosomal gene loci and integrating a variety of DNA sequences.
DERWENT CLASS: B04 D16
INVENTOR(S): BREITLING, F; KUHLWEIN, T; MOLDENHAUER, G; POUSTKA, A; KUEHLWEIN, T
PATENT ASSIGNEE(S): (DEKR-N) DEUT KREBSFORSCHUNGSZENT STIFTUNG; (DEKR-N) DEUT KREBSFORSCHUNGSZENTRUM
COUNTRY COUNT: 101
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 1298207	A1	20030402	(200337)*	GE	75
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
WO 2003029458	A2	20030410	(200337)	GE	
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM					
AU 2002338816	A1	20030414	(200460)		
JP 2005503826	W	20050210	(200511)		218

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1298207	A1	EP 2001-123596	20011001
WO 2003029458	A2	WO 2002-EP10852	20020927
AU 2002338816	A1	AU 2002-338816	20020927
JP 2005503826	W	WO 2002-EP10852	20020927
		JP 2003-532674	20020927

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002338816	A1	Based on	WO 2003029458
JP 2005503826	W	Based on	WO 2003029458

PRIORITY APPLN. INFO: EP 2001-123596 20011001
AN 2003-383833 [37] WPIDS
AB EP 1298207 A UPAB: 20030612
NOVELTY - Preparing (M1) a library (A) of protein-producing eukaryotic cells (B).

(a) Introducing specific recombination signals (RS) into one or two chromosomal gene loci (II);

(b) Expanding at least one of the modified cells;

(c) Transfecting many different DNA sequences (I), each flanked by RS, into the expanded cells; and

(d) Integrating (I) into (II) on the basis of RS and the appropriate recombinase.

DETAILED DESCRIPTION - Preparing a library (A) of protein-producing eukaryotic cells (B) comprises:

(a) Introducing specific recombination signals (RS) into one or two chromosomal gene loci in the cells;

(b) Expanding at least one of the modified cell;

(c) Transfecting many different DNA sequences (I), each flanked by RS, into the expanded cells and

(d) Integrating (I) into the gene loci on the basis of RS and the appropriate recombinase.

The resulting cells express different proteins (II), each from an integrated (I), and (II) are bound to the cell surface.

INDEPENDENT CLAIMS are also included for:

(1) Library (A) produced by (M1);

(2) Isolating (M2) monoclonal antibodies (MAb) of the required specificity by incubating (A) with an antigen (Ag) and isolating those cells where Ag binds to the surface;

(3) Humanizing hybridomas (M3);

(4) Vector (III) containing one or more (I); and

(5) Host cell containing (III).

USE - For preparing a library of protein-producing eukaryotic cells (Claimed). The method is particularly used to produce libraries of humanized monoclonal antibodies, for selection of those with affinity for particular antigens and useful for diagnostic or therapeutic use. Libraries of T cell receptors may also be prepared.

ADVANTAGE - The method produces libraries of high diversity; provides easy, quick and automatable selection from a large number of proteins; allows relatively simple alteration of the expressed gene (e.g. fusion to other protein-coding sequences); is suitable for large scale protein production; and allows simple verification and characterization of selected cell lines. The method does not require incorporation of a resistance marker.

Dwg.0/18

L39 ANSWER 22 OF 25 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2002-635678 [68] WPIDS

CROSS REFERENCE: 2004-051016 [05]

DOC. NO. CPI: C2004-013425

TITLE: Novel nucleotide construct useful for disrupting function of gene in embryonic stem cell, comprises sequence encoding positive selection marker flanked by restriction enzyme sites, to create a single-stranded region.

DERWENT CLASS: B04 D16

INVENTOR(S): BRENNAN, T J; KLEIN, R D

PATENT ASSIGNEE(S): (DELT-N) DELTAGEN INC; (BREN-I) BRENNAN T J; (KLEI-I) KLEIN R D

COUNTRY COUNT: 1

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2002086369	A1	20020704	(200268)*		37
US 6815185	B2	20041109	(200474)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 2002086369	A1	Provisional	US 1997-84194P	19971117
		Provisional	US 1998-84949P	19980511
		Cont of	US 1998-193834	19981117
			US 2001-885816	20010619
US 6815185	B2	Provisional	US 1997-84194P	19971117

Provisional	US 1998-84949P	19980511
Cont of	US 1998-193834	19981117
	US 2001-885816	20010619

PRIORITY APPLN. INFO: US 2001-885816 20010619; US 1997-84194P 19971117; US 1998-84949P 19980511; US 1998-193834 19981117

AN 2002-635678 [68] WPIDS
CR 2004-051016 [05]
AB US2002086369 A UPAB: 20041117

NOVELTY - A nucleotide construct (I) comprising a sequence encoding positive selection marker flanked by restriction enzyme sites, the restriction enzyme sites flanked by sequences which are not complementary to each other and which do not include at least one type of base at any position, where the construct is treated so that single-stranded regions are created at each sequence lacking at least one nucleotide, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) making (M) (I);
(2) a targeting construct produced by the method of (1);
(3) a host cell containing (I); and
(4) an animal or plant cell containing (I).

USE - (I) is useful for disrupting the function of a target sequence or gene in a cell e.g. embryonic stem cell, by inserting sequences homologous to the target gene into the construct such that the sequences **homologous** to the target gene **flank** the positive selection marker, to produce a targeting construct, and introducing the targeting construct into the cell to produce a homologous recombinant and thus the function of the target gene or sequence is disrupted. The homologous sequences are sequences flanking the site in the target gene that is to be disrupted. The method further comprises enriching for the homologous recombinant having the target gene or sequence disrupted, where the enrichment step comprises screening cells containing the targeting construct, under ultraviolet light and identifying cells that do not fluoresce. (All claimed). (I) is useful in a rapid and efficient method for generating DNA constructs suitable for introducing into embryonic stem cells. (I) is useful for deleting or mutating a specific gene in the target animal. (I) is utilized in conventional techniques of molecular biology, microbiology, cell biology and recombinant DNA.

ADVANTAGE - (I) eliminates the need for the traditional hybridization isolation of a single genomic clone, restriction mapping of the clone and multiple cloning steps. (M) is fast and efficiently generates nucleotide construct, and reduces the time required for making a knock-out vector. Isolating an individual genomic clone or mapping the restriction sites within the clone is not needed for (M). (M) is ligation independent cloning.

Dwg.0/8

L39 ANSWER 23 OF 25 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER:	2002-424755 [45] WPIDS
DOC. NO. CPI:	C2002-120270
TITLE:	Screening DNA library for selected gene, useful e.g. for creating knockout animals, based on homologous recombination with sequence that includes a positive selection marker.
DERWENT CLASS:	B04 C06 D16
INVENTOR(S):	ELLEDGE, S J; LI, M; ZHANG, P
PATENT ASSIGNEE(S):	(BAYU) BAYLOR COLLEGE MEDICINE
COUNTRY COUNT:	23
PATENT INFORMATION:	

PATENT NO	KIND	DATE	WEEK	LA	PG
US 6376192	B1	20020423	(200245)*		22
WO 2002044415	A1	20020606	(200245)	EN	
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
W: AU CA JP					
AU 2002019856	A	20020611	(200264)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 6376192	B1	US 2000-724934	20001128
WO 2002044415	A1	WO 2001-US44088	20011127
AU 2002019856	A	AU 2002-19856	20011127

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002019856	A	Based on	WO 2002044415

PRIORITY APPLN. INFO: US 2000-724934 20001128

AN 2002-424755 [45] WPIDS

AB US 6376192 B UPAB: 20021031

NOVELTY - Screening a DNA library for a selected gene (I) by co-transforming Escherichia coli with a representative part of a library and a nucleic acid fragment (II) encoding a positive selection marker (PSM) flanked by fragments homologous with sequences present in (I), is new. The cell is incubated to allow (II) to recombine into (I), and grown under selective conditions to identify recombination events.

DETAILED DESCRIPTION - Screening a DNA library for a selected gene (I) by co-transforming Escherichia coli with a representative part of the library and a nucleic acid fragment (II) encoding a positive selection marker (PSM) flanked by fragments homologous with sequences present in (I), is new. The cell is incubated to allow (II) to recombine into (I), then grown under selective conditions to identify recombination events. The host cells express the exo and beta -recombination functions of lambda phage.

INDEPENDENT CLAIMS are also included for the following:

(1) preparing a targeting vector (TV) for preparation of mammalian embryonic stem cells (ESC) in which (I) is disrupted, and thus of knockout mammals; and

(2) screening a library for a selected nucleic acid (Ia).

USE - The method is used to isolate particular genes (especially from large libraries), particularly for making vectors that target selected genes and are used to generate knockout mammals, but it can also be used to extend partial sequences or to fill in gaps in sequences.

ADVANTAGE - The method makes possible identification of genes based on only 60-100 bases of homology, because homologous recombination introduces a selection marker essential for cell survival on selection media. A library can now be screened, and transfer vector prepared, in 1 week, months can be required in current methods, specifically plaque-lifts and polymerase chain reactions are not needed.

Dwg.0/8

L39 ANSWER 24 OF 25 WPIDS

ACCESSION NUMBER: 2002-164642 [21] WPIDS

DOC. NO. CPI: C2002-050915

TITLE: Novel nucleotide construct for generating DNA constructs for introducing into embryonic stem cell, comprising a

sequence encoding a positive selection marker flanked by restriction enzyme sites.

DERWENT CLASS: B04 D16
INVENTOR(S): BRENNAN, T J; KLEIN, R D
PATENT ASSIGNEE(S): (DELT-N) DELTAGEN INC
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002004621	A2	20020117	(200221)*	EN	64
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000060840	A	20020121	(200234)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002004621	A2	WO 2000-US18812	20000711
AU 2000060840	A	AU 2000-60840	20000711
		WO 2000-US18812	20000711

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000060840	A	Based on	WO 2002004621

PRIORITY APPLN. INFO: WO 2000-US18812 20000711
AN 2002-164642 [21] WPIDS
AB WO 200204621 A UPAB: 20020403
NOVELTY - A nucleotide construct (I) comprising a sequence encoding a positive selection marker flanked by restriction enzyme sites (RS), where RS is flanked by sequences which are not complementary to each other and which do not include at least one type of base at any position, where the construct can be treated so that single-stranded regions are created at each sequence lacking at least one nucleotide, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) making (M1) a DNA construct useful in introducing a nucleotide sequence into a target DNA, by:

(a) amplifying in one reaction, a first polynucleotide comprising two different nucleotide sequences substantially homologous to the target DNA, and inserting a second polynucleotide between the two different nucleotide sequences; or

(b) providing a polynucleotide substantially homologous to the target DNA, generating two different fragments of the polynucleotide, providing a vector having a gene encoding for a positive selection marker, and using ligation independent cloning to insert the two different fragments into the vector to form the construct, where the positive selection marker is between the two different sequence fragments in the construct;

(2) disrupting (M2) the function of a target sequence or gene in a cell, by inserting sequences homologous to the target gene into (I), such that the sequences **homologous** to the target gene **flank** the positive selection marker, to produce a targeting construct, and introducing the targeting construct into the cell to produce a homologous recombinant, where the function of the target gene or sequence is

disrupted;
(3) a targeting construct (II) produced by (M1);
(4) a host cell containing (I) or (II); and
(5) an animal or plant containing (II).
USE - (I) is useful in a rapid and efficient method for generating DNA constructs suitable for introduction into embryonic stem cells.
ADVANTAGE - The methods using (I) eliminates the need for the traditional hybridization isolation of a single genomic clone, restriction mapping of the cloned and multiple cloning steps. (I) is generated without isolating an individual genomic clone or mapping the restriction sites within the clone. M1 is fast and efficient in making (I). The method provides an unexpected reduction in the time required for making a knock-out vector (within 1-2 weeks) where the conventional methods require 2-4 months.
DESCRIPTION OF DRAWING(S) - The figure shows the method of constructing a targeting vector.
Dwg.1/7

L39 ANSWER 25 OF 25 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-171130 [15] WPIDS
DOC. NO. CPI: C2000-053234
TITLE: Screening for interactions between human beta amyloid precursor protein and human lon-protease like protein, useful for treating neurodegenerative disease.
DERWENT CLASS: B04 D16
INVENTOR(S): NANDABALAN, K; SCHULZ, V P; YANG, M
PATENT ASSIGNEE(S): (CURA-N) CURAGEN CORP
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000002911	A2	20000120	(200015)*	EN	69
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9948693	A	20000201	(200028)		
EP 1095154	A2	20010502	(200125)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2002521004	W	20020716	(200261)		103

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000002911	A2	WO 1999-US15592	19990708
AU 9948693	A	AU 1999-48693	19990708
EP 1095154	A2	EP 1999-932376	19990708
		WO 1999-US15592	19990708
JP 2002521004	W	WO 1999-US15592	19990708
		JP 2000-559140	19990708

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9948693	A	Based on	WO 2000002911
EP 1095154	A2	Based on	WO 2000002911

JP 2002521004 W Based on WO 2000002911

PRIORITY APPLN. INFO: US 1998-113348 19980710
AN 2000-171130 [15] WPIDS
AB WO 200002911 A UPAB: 20000323
NOVELTY - A novel interaction between beta -amyloid precursor protein (beta -APP) (I) and the human lon-protease like protein (HsLON) (II) is new. The complex formed is implicated in modulating the functional activities of (I) and its binding partner.

DETAILED DESCRIPTION - New purified complex (C) of (I) and (II) in which the proteins involved may be derivative of (I) and (II).

INDEPENDENT CLAIMS are also included for the following:

(1) a chimeric protein comprising a fragment of (I) consisting of at least 6 amino acids (aa) fused via a covalent bond to a fragment of (II) consisting of at least 6 aas, where the fragments are capable of binding each other to form a complex;

(2) an antibody which binds C, but does not bind any part of (I) or (II) that is not part of C;

(3) an isolated nucleic acid (NA), or a combination of NAs, encoding (I) and (II);

(4) an isolated NA encoding the protein of (1);

(5) a cell containing the recombinant NAs of (3) and (4);

(6) a composition comprising C, the protein of (1) the antibody of (2), the NAs of (3) or (4), or the cells of (5);

(7) producing C, comprising growing a recombinant cell containing the NA of (3), such that the proteins are expressed and bind to each other, and recovering the expressed C;

(8) diagnosing or screening for the presence of or a disposition for developing a disease or disorder characterized by an aberrant level of C, comprising measuring the:
(a) level of C;

(b) RNA encoding (I) and (II), or

(c) functional activity of C in a sample obtained from the subject; in which a increase or decrease in the level of one (a)-(c) in the sample, relative to the level of (a)-(c) in a normal sample indicates the presence of the disease or a predisposition for the disease;

(9) treating or preventing a disease or disorder involving aberrant levels of C in a subject, comprising administering molecules that modulate the function of C;

(10) treating or preventing a disease or disorder involving an aberrant level of (I) or (II) in a subject by administering a molecule that modulates the function of (I) or (II);

(11) screening for purified C, or a derivative of C, or a modulator of the activity of C for activity in treating or preventing neurodegenerative disease, cardiomyopathy, a diabetes, a hearing loss, male infertility, or mitochondrial DNA mutation associated disorders, comprising contacting cultured cells that exhibit an indicator of the disease or disorder in vitro with the C, derivative or modulator, and comparing the level of the indicator in contacted cells with non-contacted cells, where a lower level in the contacted cells indicates that the C, derivative or analog has activity in treating or preventing the disease;

(12) screening for or identifying a molecule that modulates the formation of C, comprising measuring the levels of C formed from (I) and (II) in the presence and absence of the molecule;

(13) a recombinant non-human animal in which both an endogenous (I) gene and (II) gene have been deleted or inactivated by homologous recombination or insertional mutagenesis;

(14) a recombinant non-human animal containing a (I) gene and (II) gene, both under the control of promoter that are non native (I) and (II) promoters;

(15) a recombinant non-human animal containing a transgene comprising a NA encoding the protein of (1);

(16) modulating the activity or levels of (I) or (II), by contacting a cell with a gene expressing the protein, or NA encoding the protein, or an antibody that binds the protein;

(17) identifying a molecule that modulates the activity of C by contacting a cell with a molecule that modulates the formation of C;

(18) monitoring the efficacy of a treatment of a disease or disorder characterized by an aberrant level of C, comprising measuring the:

(a) as in (8a) and (8b), and

(b) functional activity of C in samples taken before and after treatment, where a change or lack or change indicates whether the treatment is effective.

USE - The complex formed by the interaction of beta - amyloid precursor protein (beta -APP) and the human lon- protease like protein (HsLON) may serve as a marker for specific disease states that involve the disruption of physiological processes in which beta -APP and HsLON are known to be involved. Methods of screening for these complexes are used to treat and/or prevent diseases including, but are not limited to, neurodegenerative disorders (claimed) such as Alzheimer's disease, dementia of trisomy 21, Parkinson's disease, amylotrophic lateral sclerosis (ALS); cardiomyopathy (claimed); some forms of diabetes (claimed); hearing loss (claimed); male infertility (claimed); and disorders associated with mitochondrial DNA mutations (claimed). The complexes have diagnostic utility for these diseases. Detection of the complexes may be utilized in the analysis of various diseases, prognosis, identifying disease states, following a disease course, following the efficacy of therapeutics and following therapeutic response. The nuclei acid may also be utilized for these purposes, as well as for gene therapy. Antisense sequences or ribozymes may be used to reduce formation of the complexes.

ADVANTAGE - None given.

Dwg.0/3

=> logoff y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	218.73	329.24

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-10.95	-12.41

STN INTERNATIONAL LOGOFF AT 12:29:47 ON 11 MAR 2005

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1639MLS

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	SEP 01	New pricing for the Save Answers for SciFinder Wizard within STN Express with Discover!
NEWS	4	OCT 28	KOREAPAT now available on STN
NEWS	5	NOV 30	PHAR reloaded with additional data
NEWS	6	DEC 01	LISA now available on STN
NEWS	7	DEC 09	12 databases to be removed from STN on December 31, 2004
NEWS	8	DEC 15	MEDLINE update schedule for December 2004
NEWS	9	DEC 17	ELCOM reloaded; updating to resume; current-awareness alerts (SDIs) affected
NEWS	10	DEC 17	COMPUAB reloaded; updating to resume; current-awareness alerts (SDIs) affected
NEWS	11	DEC 17	SOLIDSTATE reloaded; updating to resume; current-awareness alerts (SDIs) affected
NEWS	12	DEC 17	CERAB reloaded; updating to resume; current-awareness alerts (SDIs) affected
NEWS	13	DEC 17	THREE NEW FIELDS ADDED TO IFIPAT/IFIUDB/IFICDB
NEWS	14	DEC 30	EPFULL: New patent full text database to be available on STN
NEWS	15	DEC 30	CAPLUS - PATENT COVERAGE EXPANDED
NEWS	16	JAN 03	No connect-hour charges in EPFULL during January and February 2005
NEWS	17	FEB 25	CA/CAPLUS - Russian Agency for Patents and Trademarks (ROSPATENT) added to list of core patent offices covered
NEWS	18	FEB 10	STN Patent Forums to be held in March 2005
NEWS	19	FEB 16	STN User Update to be held in conjunction with the 229th ACS National Meeting on March 13, 2005
NEWS	20	FEB 28	PATDPAFULL - New display fields provide for legal status data from INPADOC
NEWS	21	FEB 28	BABS - Current-awareness alerts (SDIs) available
NEWS	22	FEB 28	MEDLINE/LMEDLINE reloaded
NEWS	23	MAR 02	GBFULL: New full-text patent database on STN
NEWS	24	MAR 03	REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS	25	MAR 03	MEDLINE file segment of TOXCENTER reloaded

NEWS EXPRESS	JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and News Items
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN
NEWS WWW	CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that

specific topic.

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FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005

=> fil medline biosis caplus embase wpids

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 11:08:23 ON 11 MAR 2005

FILE 'BIOSIS' ENTERED AT 11:08:23 ON 11 MAR 2005
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FILE 'WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005
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=> initiat (w) DNA (w) uptake
MISSING TERM BEFORE '(W'
Search expressions cannot begin with operators.

=> initiat? (w) DNA (w) uptake
L1 0 INITIAT? (W) DNA (W) UPTAKE

=> initiat? (s) DNA (s) uptake
L2 373 INITIAT? (S) DNA (S) UPTAKE

=> non (w) homologous
L3 4746 NON (W) HOMOLOGOUS

=> l2 and l3
L4 0 L2 AND L3

=> d scan l3

L3 4746 ANSWERS BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI The Saccharomyces cerevisiae PDS1 and RAD9 checkpoint genes control different DNA double-strand break repair pathways.
IT Miscellaneous Descriptors
DNA damage; UV radiation; X ray; **non-homologous** end joining; signal transduction; single-strand annealing

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):end

=> d scan l2

```
L2    373 ANSWERS   CAPLUS  COPYRIGHT 2005 ACS on STN
CC    14-6 (Mammalian Pathological Biochemistry)
TI    Genetic regulation of the androgen receptor.  Testicular feminization in
      the mouse
ST    testicular feminization androgen receptor gene
IT    Receptors
      RL: BIOL (Biological study)
         (for androgens, in testicular feminization, genes in relation to)
IT    Androgenic hormones
      RL: BSU (Biological study, unclassified); BIOL (Biological study)
         (receptors, in testicular feminization, genes in relation to)
IT    Testis, disease or disorder
         (testicular feminization, androgen receptor in, gene in relation to)
IT    Gene
      RL: BIOL (Biological study)
         (testicular feminization, in testis disorder, androgen receptor in
         relation to)

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):2

L2    373 ANSWERS  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI    BINDING OF PHORBOL ESTERS TO HIGH AFFINITY SITES ON MURINE FIBROBLASTIC
      CELLS ELICITS A MITOGENIC RESPONSE.
IT    Miscellaneous Descriptors
         TUMOR PROMOTER EPIDERMAL GROWTH FACTOR RUBIDIUM-86 UPTAKE 2 DEOXY
         GLUCOSE UPTAKE DNA SYNTHESIS

L2    373 ANSWERS   CAPLUS  COPYRIGHT 2005 ACS on STN
CC    13-6 (Mammalian Biochemistry)
      Section cross-reference(s): 7
TI    Initiation of DNA synthesis by human thrombin:  relationships between
      receptor binding, enzymic activity, and stimulation of rubidium-86 ion
      influx
ST    DNA formation fibroblast thrombin ATPase
IT    Fibroblast
         (ATPase of, of laboratory animal, thrombin of human stimulation of, DNA
         formation in relation to)
IT    Receptors
      RL: BIOL (Biological study)
         (for thrombin of human, on fibroblast of laboratory animal, thrombin binding
         to, stimulation of DNA formation and ATPase in relation to)
IT    Deoxyribonucleic acid formation
         (thrombin of human stimulation of ATPase of fibroblast of laboratory animal
         in relation to)
IT    9000-83-3
      RL: BIOL (Biological study)
         (potassium-sodium activated, of fibroblast, thrombin of human
         stimulation of, DNA formation in relation to)
IT    9002-04-4
      RL: BIOL (Biological study)
         (α-, ATPase of fibroblast of laboratory animal stimulation by, of
         human, DNA formation in relation to)

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):end

=> d his

     (FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11
     MAR 2005
L1             0 INITIAT? (W) DNA (W) UPTAKE
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L2          373 INITIAT? (S) DNA (S) UPTAKE
L3         4746 NON (W) HOMOLOGOUS
L4            0 L2 AND L3

=> stuffer and DNA
L5          209 STUFFER AND DNA

=> l5 and l2
L6            0 L5 AND L2

=> DNA (w) uptake
L7         2254 DNA (W) UPTAKE

=> l7 and l3
L8            1 L7 AND L3

=> d ibib abs l8

L8   ANSWER 1 OF 1     MEDLINE on STN
ACCESSION NUMBER:    81098331     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 6256602
TITLE:               Restriction and modification in B. subtilis: the role of
                     homology between donor and recipient DNA in transformation
                     and transfection.
AUTHOR:              Bron S; Luxen E; Trautner T A
SOURCE:              Molecular & general genetics : MGG, (1980) 179 (1) 111-7.
                     Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY:        GERMANY, WEST: Germany, Federal Republic of
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         198103
ENTRY DATE:          Entered STN: 19900316
                     Last Updated on STN: 19900316
                     Entered Medline: 19810324
AB   Non-modified DNAs from phages SPO2 and phi 105, and prophage DNAs
     extracted from lysogens carrying these phages, were used to transfect
     isogenic r+m+ B. subtilis recipients which were either non-lysogenic, or
     had been lysogenized with a homologous or a non-
     homologous phage.  Restriction of transfecting phage and prophage
     DNA occurred in non-lysogenic recipients and in recipients lysogenic for a
     non-homologous phage.  No effect of restriction was
     observed when phage or prophage DNA was used to transfect recipients
     carrying a homologous prophage.  This is analogous to the absence of
     restriction in transformation and indicates that in B. subtilis the
     distinction between transforming and transforming and transfecting DNA is
     not made at the initial stages of DNA uptake and
     processing, but rather at later stages, where recognition of homologous
     regions in donor and recipient DNA plays an important role.


=> d his

     (FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11
     MAR 2005
L1            0 INITIAT? (W) DNA (W) UPTAKE
L2          373 INITIAT? (S) DNA (S) UPTAKE
L3         4746 NON (W) HOMOLOGOUS
L4            0 L2 AND L3
L5          209 STUFFER AND DNA
```

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L6            0 L5 AND L2
L7         2254 DNA (W) UPTAKE
L8            1 L7 AND L3

=> l5 and l7
L9            0 L5 AND L7

=> DNA (s) uptake
L10       18629 DNA (S) UPTAKE

=> l10 and l5
L11           0 L10 AND L5

=> l10 and l3
L12           7 L10 AND L3

=> dup rem l12
PROCESSING COMPLETED FOR L12
L13           4 DUP REM L12 (3 DUPLICATES REMOVED)

=> t ti l13 1-4

L13  ANSWER 1 OF 4     MEDLINE on STN                    DUPLICATE 1
TI   Cell to cell transmission of donor DNA overcomes differential
     incorporation of non-homologous and homologous markers
     in Neisseria gonorrhoeae.

L13  ANSWER 2 OF 4  EMBASE  COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
     on STN
TI   Cloning and characterization of the transport modifier RS1 from rabbit
     which was previously assumed to be specific for Na+-D-glucose cotransport.

L13  ANSWER 3 OF 4  EMBASE  COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
     on STN
TI   Analyzing the structures, functions and evolution of two abundant
     gastrointestinal fatty acid binding proteins with recombinant DNA and
     computational techniques.

L13  ANSWER 4 OF 4     MEDLINE on STN
TI   Restriction and modification in B. subtilis: the role of homology between
     donor and recipient DNA in transformation and transfection.


=> d ibib abs l13 1-4

L13  ANSWER 1 OF 4     MEDLINE on STN                    DUPLICATE 1
ACCESSION NUMBER:   2000033560     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 10564824
TITLE:              Cell to cell transmission of donor DNA overcomes
                    differential incorporation of non-
                    homologous and homologous markers in Neisseria
                    gonorrhoeae.
AUTHOR:             Hill S A
CORPORATE SOURCE:   Department of Biological Sciences, Northern Illinois
                    University, DeKalb, IL, USA.. sahill@niu.edu
SOURCE:             Gene, (1999 Nov 15) 240 (1) 175-82.
                    Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY:       Netherlands
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200001
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ENTRY DATE: Entered STN: 20000124
Last Updated on STN: 20000124
Entered Medline: 20000111

AB The neisseriae are naturally competent for DNA transformation. This genetic study examines whether the modification status of chromosomal donor DNA affects transformation of Neisseria gonorrhoeae to drug resistance. When a single modification system was inactivated, unmodified chromosomal donor DNA was not restricted when used to transform the cognate restriction+ host, irrespective of whether the donor DNA carried a point mutation (homologous marker) or a drug-resistance gene cassette (**non-homologous** marker). These observations contrasted transformations performed with unmodified plasmid donor DNAs, where the incoming DNA was excluded. However, during the study, it became apparent that certain strains of gonococci showed differential incorporation of **non-homologous** markers when compared with the incorporation of the homologous marker, even when the donor DNAs were prepared from parental strains. Differential incorporation of markers could be rescued either through cell to cell transmission of donor DNA, or by performing in vitro transformations with donor DNA preparations that were obtained from spent culture supernatants. Overall, the data indicate that, in addition to the exclusion of foreign **DNA** through the requirement for a genus-specific **uptake** sequence, gonococci appear capable of excluding **DNA** on the basis of homology.

L13 ANSWER 2 OF 4 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 1999061593 EMBASE
TITLE: Cloning and characterization of the transport modifier RS1 from rabbit which was previously assumed to be specific for Na+-D-glucose cotransport.
AUTHOR: Reinhardt J.; Veyhl M.; Wagner K.; Gambaryan S.; Dekel C.; Akhoundova A.; Korn T.; Koepsell H.
CORPORATE SOURCE: H. Koepsell, Anatomisches Inst., Bayerischen Julius-Maximilians-Univ., Koellikerstr. 6, Wurzburg, Germany. anat010@rzbox.uni-wuerzburg.de
SOURCE: Biochimica et Biophysica Acta - Biomembranes, (1999) 1417/1 (131-143).
Refs: 25
ISSN: 0005-2736 CODEN: BBBMBS
PUBLISHER IDENT.: S 0005-2736(98)00250-8
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 002 Physiology
029 Clinical Biochemistry
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Previously we cloned membrane associated polypeptides from pig and man (pRS1, hRS1) which altered rate and glucose dependence of Na+-d-glucose cotransport expressed by SGLT1 from rabbit and man. This paper describes the cloning of a related cDNA sequence from rabbit intestine (rbRS1) which encodes a gene product with about 65% amino acid identity to pRS1 and hRS1. Hybridization of endonuclease-restricted genomic **DNA** with cDNA fragments of rbRS1 showed that there is only one gene with similarity to rbRS1 in rabbit, and genomic PCR amplifications revealed that the rbRS1 gene is intronless. Comparing the transcription of rbRS1 and rbSGLT1 in various tissues and cell types, different mRNA patterns were obtained for both genes. In Xenopus oocytes the V(max) of expressed Na+-d-glucose cotransport was increased or decreased when rbRS1 was coexpressed with rbSGLT1 or hSGLT1, respectively. After coexpression with hSGLT1 the glucose dependence of the expressed transport was changed. By coexpression of rbRS1 with the human organic cation transporter hOCT2 the expressed

cation **uptake** was not altered; however, the expressed cation **uptake** was drastically decreased when hRS1 was coexpressed with hOCT2. The data show that RS1 can modulate the function of transporters with **non-homologous** primary structures. Copyright (C) 1999 Elsevier Science B.V.

L13 ANSWER 3 OF 4 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 85226303 EMBASE
DOCUMENT NUMBER: 1985226303
TITLE: Analyzing the structures, functions and evolution of two abundant gastrointestinal fatty acid binding proteins with recombinant DNA and computational techniques.
AUTHOR: Gordon J.L.; Lowe J.B.
CORPORATE SOURCE: Department of Biological Chemistry, Washington University School of Medicine, St. Louis, MO 63110, United States
SOURCE: Chemistry and Physics of Lipids, (1985) 38/1-2 (137-158). CODEN: CPLIA4
COUNTRY: Netherlands
DOCUMENT TYPE: Journal
FILE SEGMENT: 029 Clinical Biochemistry
048 Gastroenterology
022 Human Genetics
LANGUAGE: English
AB The structures of intestinal and liver fatty acid binding proteins (FABPs) have been determined from an analysis of the nucleotide sequences of cloned cDNAs. The primary translation product of intestinal FABP mRNA contains 132 residues (M(r)=15 124). Liver FABP mRNA encodes a 127 amino acid polypeptide (M(r)=14 273). In vitro co-translational cleavage and translocation assays showed that neither sequence has a cleavable signal peptide or signal peptide equivalent - suggesting that the FABPs do not enter the secretory apparatus but rather are targeted to the cytoplasm. A variety of computational techniques were used to compare the two FABP sequences. The results indicate that liver and intestinal FABP are paralogous homologues. A superfamily of proteins was defined which includes the FABPs, the cellular retinol and retinoic acid binding proteins, the P2 protein of peripheral nerve myelin, and a polypeptide known as 422 whose synthesis is induced during differentiation of 3T3-L1 cells to adipocytes. No sequence homologies were noted between any of these small molecular weight cytosolic proteins and nonspecific lipid transfer protein (sterol carrier protein 2), phosphatidylcholine transfer protein, serum albumin or apolipoprotein AI. The FABPs may have structural features responsible for lipid-protein interactions that are not present in these **non-homologous** sequences. The distribution of intestinal and liver FABP mRNAs in adult rat tissues and the changes in FABP gene expression which occur during gastrointestinal development support the notion that these proteins are involved in fatty acid **uptake**, transport and/or compartmentalization. However, differences in tissue distribution and periods of non-coordinate expression during gastrointestinal ontogeny suggest that the two FABPs have distinct functions. The relationship between intestinal and liver FABPs and similar sized cytosolic FABPs isolated from brain, skeletal and cardiac muscle remains unclear. Recombinant **DNA** techniques combined with comparative sequence analysis offer a useful approach for defining unique as well as general structure-function relationships in this group of fatty acid binding proteins.

L13 ANSWER 4 OF 4 MEDLINE on STN
ACCESSION NUMBER: 81098331 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6256602
TITLE: Restriction and modification in B. subtilis: the role of homology between donor and recipient DNA in transformation

and transfection.
AUTHOR: Bron S; Luxen E; Trautner T A
SOURCE: Molecular & general genetics : MGG, (1980) 179 (1) 111-7.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198103
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19900316
Entered Medline: 19810324

AB Non-modified DNAs from phages SPO2 and phi 105, and prophage DNAs extracted from lysogens carrying these phages, were used to transfect isogenic r+m+ B. subtilis recipients which were either non-lysogenic, or had been lysogenized with a homologous or a **non-homologous** phage. Restriction of transfecting phage and prophage DNA occurred in non-lysogenic recipients and in recipients lysogenic for a **non-homologous** phage. No effect of restriction was observed when phage or prophage DNA was used to transfect recipients carrying a homologous prophage. This is analogous to the absence of restriction in transformation and indicates that in B. subtilis the distinction between transforming and transforming and transfecting **DNA** is not made at the initial stages of **DNA** **uptake** and processing, but rather at later stages, where recognition of homologous regions in donor and recipient **DNA** plays an important role.

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

L1 0 INITIAT? (W) DNA (W) UPTAKE
L2 373 INITIAT? (S) DNA (S) UPTAKE
L3 4746 NON (W) HOMOLOGOUS
L4 0 L2 AND L3
L5 209 STUFFER AND DNA
L6 0 L5 AND L2
L7 2254 DNA (W) UPTAKE
L8 1 L7 AND L3
L9 0 L5 AND L7
L10 18629 DNA (S) UPTAKE
L11 0 L10 AND L5
L12 7 L10 AND L3
L13 4 DUP REM L12 (3 DUPLICATES REMOVED)

=> e diaz (w) torres maria/au
E1 1 DIAYE M R/AU
E2 10 DIAZ/AU
E3 0 --> DIAZ (W) TORRES MARIA/AU
E4 1094 DIAZ A/AU
E5 29 DIAZ A A/AU
E6 1 DIAZ A AGUIRRE/AU
E7 2 DIAZ A ANTONIO/AU
E8 3 DIAZ A B/AU
E9 1 DIAZ A B P/AU
E10 17 DIAZ A C/AU
E11 1 DIAZ A C L/AU
E12 2 DIAZ A CARRO/AU

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=> e diaz torres maria/au
E1          30     DIAZ TORRES M R/AU
E2           2     DIAZ TORRES MARI/AU
E3           5 --> DIAZ TORRES MARIA/AU
E4          17     DIAZ TORRES MARIA R/AU
E5           2     DIAZ TORRES MARTHA L/AU
E6           1     DIAZ TORRES MIGUEL ANGEL/AU
E7           1     DIAZ TORRES N J/AU
E8           1     DIAZ TORRES RAUL/AU
E9           2     DIAZ TORRES Y/AU
E10          3     DIAZ TORRES YANETH/AU
E11          1     DIAZ TORREZ M/AU
E12          1     DIAZ TORREZ R/AU

=> e1-34
'E34' NOT FOUND
The E# entered is not currently defined.

=> e1-e4
L14         54 ("DIAZ TORRES M R"/AU OR "DIAZ TORRES MARI"/AU OR "DIAZ TORRES
               MARIA"/AU OR "DIAZ TORRES MARIA R"/AU)

=> dup rem l14
PROCESSING COMPLETED FOR L14
L15          23 DUP REM L14 (31 DUPLICATES REMOVED)

=> transform? and l15
L16          2 TRANSFORM? AND L15

=> t ti l15 1-23

L15  ANSWER 1 OF 23  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   Production of secreted polypeptides.

L15  ANSWER 2 OF 23  CAPLUS  COPYRIGHT 2005 ACS on STN DUPLICATE 1
TI   Bacillus transformation and construction of mutant libraries

L15  ANSWER 3 OF 23  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   Enhancing growth in gram-positive microorganisms using formate
     supplementation and inactivation of formate-associated transport proteins.

L15  ANSWER 4 OF 23  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Production of secreted polypeptides in bacteria expressing mutant peptide
     transport protein encoded by oppA or dciA operon

L15  ANSWER 5 OF 23  CAPLUS  COPYRIGHT 2005 ACS on STN DUPLICATE 2
TI   Method for improving protein production in gram-positive microorganisms by
     inactivating opp operon gene products

L15  ANSWER 6 OF 23  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   Method for the recombinant production of 1,3-propanediol.

L15  ANSWER 7 OF 23  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   Method for the production of 1,3-propanediol by recombinant
     microorganisms.

L15  ANSWER 8 OF 23  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Bacillus molecules associated with formate transport (FTAP 1, FTAP 2, PurU
     and FMD), sequences and use in modifying microbial growth and obtaining
     Bacillus capable of generating recombinant protein
```

L15 ANSWER 9 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Proteome analysis of biofilms: Growth of Bacillus subtilis on solid medium as model.

L15 ANSWER 10 OF 23 MEDLINE on STN DUPLICATE 3
TI Proteome analysis of biofilms: growth of Bacillus subtilis on solid medium as model.

L15 ANSWER 11 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
TI Method for the recombinant production of 1,3-propanediol using protein X, protein 1, protein 2, and protein 3 for dehydratase reactivation

L15 ANSWER 12 OF 23 MEDLINE on STN DUPLICATE 4
TI Solid medium labeling applied to two-dimensional gel electrophoresis.

L15 ANSWER 13 OF 23 MEDLINE on STN DUPLICATE 5
TI Identification and cloning of a mobile transposon from Aspergillus niger var. awamori.

L15 ANSWER 14 OF 23 MEDLINE on STN DUPLICATE 6
TI Analysis of the altered mRNA stability (ams) gene from Escherichia coli. Nucleotide sequence, transcriptional analysis, and homology of its product to MRP3, a mitochondrial ribosomal protein from Neurospora crassa.

L15 ANSWER 15 OF 23 MEDLINE on STN DUPLICATE 7
TI Extracellular release of protease III (ptr) by Escherichia coli K12.

L15 ANSWER 16 OF 23 MEDLINE on STN DUPLICATE 8
TI Transcriptional antitermination in the bgl operon of E. coli is modulated by a specific RNA binding protein.

L15 ANSWER 17 OF 23 MEDLINE on STN DUPLICATE 9
TI Cloning of the altered mRNA stability (ams) gene of Escherichia coli K-12.

L15 ANSWER 18 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 10
TI CHEMICAL COMPOSITION AND ULTRASTRUCTURE OF WILD-TYPE AND WHITE MUTANT ASPERGILLUS-NIDULANS CONIDIAL WALLS.

L15 ANSWER 19 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 11
TI COMPOSITION AND ULTRASTRUCTURE OF THE SPORANGIOSPORE WALL OF RHIZOPUS-STOLONIFER.

L15 ANSWER 20 OF 23 MEDLINE on STN DUPLICATE 12
TI Transcript mapping using [35S]DNA probes, trichloroacetate solvent and dideoxy sequencing ladders: a rapid method for identification of transcriptional start points.

L15 ANSWER 21 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI SECRETION OF PROTEASE III-ALKALINE PHOSPHATASE FUSION PROTEINS IN ESCHERICHIA-COLI K-12.

L15 ANSWER 22 OF 23 MEDLINE on STN DUPLICATE 13
TI Analysis of the regulatory region of the protease III (ptr) gene of Escherichia coli K-12.

L15 ANSWER 23 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 14
TI CHEMICAL COMPOSITION AND ELECTRON MICROSCOPY OF THE RODLET LAYER OF ASPERGILLUS-NIDULANS CONIDIA.

=> d ibib abs l15 1,2,6,11

L15 ANSWER 1 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:226073 BIOSIS
DOCUMENT NUMBER: PREV200300226073
TITLE: Production of secreted polypeptides.
AUTHOR(S): **Diaz-Torres, Maria R.** [Inventor, Reprint Author]
CORPORATE SOURCE: Los Gatos, CA, USA
ASSIGNEE: Genencor International, Inc.
PATENT INFORMATION: US 6544792 April 08, 2003
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Apr 8 2003) Vol. 1269, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 7 May 2003
Last Updated on STN: 7 May 2003
AB Described herein are methods and compositions for the production and secretion of polypeptides. Included herein is the use of interrupting peptide transport activity for an increase in polypeptide production and/or secretion.

L15 ANSWER 2 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2002:142863 CAPLUS
DOCUMENT NUMBER: 136:195270
TITLE: Bacillus transformation and construction of mutant libraries
INVENTOR(S): **Diaz-Torres, Maria R.**; Schellenberger, Volker; Selifonova, Olga V.; Morrison, Thomas B.; Lee, Edwin W.
PATENT ASSIGNEE(S): Genencor International, Inc., USA
SOURCE: PCT Int. Appl., 48 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002014490	A2	20020221	WO 2001-US25166	20010810
WO 2002014490	A3	20030206		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2418317	AA	20020221	CA 2001-2418317	20010810
AU 2001079254	A5	20020225	AU 2001-79254	20010810
US 2002182734	A1	20021205	US 2001-927161	20010810
EP 1309677	A2	20030514	EP 2001-957519	20010810
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRIORITY APPLN. INFO.: US 2000-224948P P 20000811
WO 2001-US25166 W 20010810

AB The present invention provides methods for building DNA constructs in vitro, transforming such constructs into competent Bacillus strains with good efficiency, and generating populations of mutants. Also provided is a method to assemble DNA constructs in situ. The invention also relates to methods for randomly mutagenizing a large DNA fragment, or the signal sequence, with an antibiotic marker and homologous DNA on either side of subtilisin gene. The invention also shows that the efficiency of transformation is increased by adding non-homologous flanks to the transforming DNA. The invention further relates to methods for performing site-directed mutagenesis on the gene of interest and directly transform Bacillus strains with the mutagenized DNA.

L15 ANSWER 6 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2001:245339 BIOSIS
DOCUMENT NUMBER: PREV200100245339
TITLE: Method for the recombinant production of 1,3-propanediol.
AUTHOR(S): **Diaz-Torres, Mari** [Inventor]; Dunn-Coleman, Nigel S. [Inventor, Reprint author]; Chase, Matthew W. [Inventor]; Trimbur, Donald [Inventor]
CORPORATE SOURCE: Los Gatos, CA, USA
ASSIGNEE: Genencor International, Inc.
PATENT INFORMATION: US 6136576 October 24, 2000
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Oct. 24, 2000) Vol. 1239, No. 4. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 23 May 2001
Last Updated on STN: 19 Feb 2002

AB The present invention provides an improved method for the production of 1,3-propanediol from a variety of carbon sources in an organism capable of 1,3-propanediol production and comprising DNA encoding protein X of a microorganismal dehydratase or protein X in combination with at least one of protein 1, protein 2 and protein 3, which proteins are comparable to those encoded by orfY, orfX and orfW, respectively from a microorganismal dha regulon. The protein X may be isolated from a diol dehydratase or a glycerol dehydratase. The present invention also provides host cells comprising protein X that are capable of increased production of 1,3-propanediol.

L15 ANSWER 11 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1998:344516 CAPLUS
DOCUMENT NUMBER: 129:24165
TITLE: Method for the recombinant production of 1,3-propanediol using protein X, protein 1, protein 2, and protein 3 for dehydratase reactivation
INVENTOR(S): Dunn-Coleman, Nigel S.; **Diaz-Torres, Maria**; Chase, Matthew W.; Trimbur, Donald
PATENT ASSIGNEE(S): Genencor International, Inc., USA; Dunn-Coleman, Nigel S.; Diaz-Torres, Maria; Chase, Matthew W.; Trimbur, Donald
SOURCE: PCT Int. Appl., 133 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9821341	A2	19980522	WO 1997-US20873	19971113
WO 9821341	A3	19980625		

W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

ZA 9710194	A	19990512	ZA 1997-10194		19971112
US 6013494	A	20000111	US 1997-968563		19971112
CA 2270906	AA	19980522	CA 1997-2270906		19971113
AU 9855076	A1	19980603	AU 1998-55076		19971113
AU 735080	B2	20010628			
EP 946732	A2	19991006	EP 1997-951433		19971113

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

CN 1239511	A	19991222	CN 1997-180074		19971113
US 6136576	A	20001024	US 1997-969683		19971113
NZ 335392	A	20001027	NZ 1997-335392		19971113
JP 2001503636	T2	20010321	JP 1998-522870		19971113
BR 9714313	A	20010918	BR 1997-14313		19971113
MX 9904337	A	20000430	MX 1999-4337		19990511
KR 2000053213	A	20000825	KR 1999-704181		19990512
US 2003022323	A1	20030130	US 1999-308207		19990513
PRIORITY APPLN. INFO.:			US 1996-30601P	P	19961113
			WO 1997-US20873	W	19971113

AB The present invention provides an improved method for the production of 1,3-propanediol from a variety of carbon sources in an organism comprising DNA encoding protein X of a dehydratase gene cluster or protein X in combination with at least one of protein 1, protein 2 and protein 3, where genes encoding these proteins are used to transform the organism and the transformed organism is cultured under appropriate conditions with a monosaccharide, oligosaccharide, or polysaccharide carbon source and a one-carbon substrate. The protein X may be isolated from a diol dehydratase or a glycerol dehydratase. The present invention also provides host cells comprising protein X that are capable of increased production of 1,3-propanediol. The invention is based, in part, upon the unexpected discovery that the presence of a protein X gene or protein X plus at least one of protein 1, protein 2, and protein 3, along with a dehydratase activity and capable of 1,3-propanediol production is associated with
in vivo reactivation of dehydratase and increased production Sequences of proteins X, 1, 2, and 3 are also claimed.

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

L1	0	INITIAT? (W) DNA (W) UPTAKE
L2	373	INITIAT? (S) DNA (S) UPTAKE
L3	4746	NON (W) HOMOLOGOUS
L4	0	L2 AND L3
L5	209	STUFFER AND DNA
L6	0	L5 AND L2
L7	2254	DNA (W) UPTAKE
L8	1	L7 AND L3
L9	0	L5 AND L7
L10	18629	DNA (S) UPTAKE
L11	0	L10 AND L5

```
L12           7 L10 AND L3
L13           4 DUP REM L12 (3 DUPLICATES REMOVED)
                E DIAZ (W) TORRES MARIA/AU
                E DIAZ TORRES MARIA/AU
L14          54 E1-E4
L15          23 DUP REM L14 (31 DUPLICATES REMOVED)
L16           2 TRANSFORM? AND L15

=> t ti l16 1-2

L16  ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Bacillus transformation and construction of mutant libraries

L16  ANSWER 2 OF 2  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Method for the recombinant production of 1,3-propanediol using protein X,
     protein 1, protein 2, and protein 3 for dehydratase reactivation


=> l3 and l5
L17           0 L3 AND L5

=> transform?
L18     1447160 TRANSFORM?

=> l3 and l18
L19         470 L3 AND L18

=> l19 and l5
L20           0 L19 AND L5

=> l19 and l10
L21           5 L19 AND L10

=> dup rem l21
PROCESSING COMPLETED FOR L21
L22           2 DUP REM L21 (3 DUPLICATES REMOVED)

=> t ti l22 1-2

L22  ANSWER 1 OF 2     MEDLINE on STN                    DUPLICATE 1
TI   Cell to cell transmission of donor DNA overcomes differential
     incorporation of non-homologous and homologous markers
     in Neisseria gonorrhoeae.

L22  ANSWER 2 OF 2     MEDLINE on STN
TI   Restriction and modification in B. subtilis: the role of homology between
     donor and recipient DNA in transformation and transfection.


=> d ibib l22 1-2

L22  ANSWER 1 OF 2     MEDLINE on STN                    DUPLICATE 1
ACCESSION NUMBER:   2000033560     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 10564824
TITLE:              Cell to cell transmission of donor DNA overcomes
                    differential incorporation of non-
                    homologous and homologous markers in Neisseria
                    gonorrhoeae.
AUTHOR:             Hill S A
CORPORATE SOURCE:   Department of Biological Sciences, Northern Illinois
                    University, DeKalb, IL, USA.. sahill@niu.edu
SOURCE:             Gene, (1999 Nov 15) 240 (1) 175-82.
```

Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000124
Last Updated on STN: 20000124
Entered Medline: 20000111

L22 ANSWER 2 OF 2 MEDLINE on STN
ACCESSION NUMBER: 81098331 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6256602
TITLE: Restriction and modification in B. subtilis: the role of homology between donor and recipient DNA in **transformation** and transfection.
AUTHOR: Bron S; Luxen E; Trautner T A
SOURCE: Molecular & general genetics : MGG, (1980) 179 (1) 111-7.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198103
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19900316
Entered Medline: 19810324

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FULL ESTIMATED COST	109.76	109.97

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CA SUBSCRIBER PRICE	-1.46	-1.46

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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Mar 4, 2005 (20050304/UP).

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

L1	0	INITIAT? (W) DNA (W) UPTAKE
L2	373	INITIAT? (S) DNA (S) UPTAKE
L3	4746	NON (W) HOMOLOGOUS
L4	0	L2 AND L3
L5	209	STUFFER AND DNA
L6	0	L5 AND L2
L7	2254	DNA (W) UPTAKE
L8	1	L7 AND L3
L9	0	L5 AND L7
L10	18629	DNA (S) UPTAKE

```
L11           0 L10 AND L5
L12           7 L10 AND L3
L13           4 DUP REM L12 (3 DUPLICATES REMOVED)
                E DIAZ (W) TORRES MARIA/AU
                E DIAZ TORRES MARIA/AU
L14          54 E1-E4
L15          23 DUP REM L14 (31 DUPLICATES REMOVED)
L16           2 TRANSFORM? AND L15
L17           0 L3 AND L5
L18     1447160 TRANSFORM?
L19         470 L3 AND L18
L20           0 L19 AND L5
L21           5 L19 AND L10
L22           2 DUP REM L21 (3 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

=> d scan l19
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The DISPLAY SCAN command is not valid in the current file.
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options in current file.

=> fil medline biosis caplus embase wpids
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                                                   ENTRY    SESSION
FULL ESTIMATED COST                                 0.54     110.51

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)    SINCE FILE      TOTAL
                                                   ENTRY    SESSION
CA SUBSCRIBER PRICE                                 0.00      -1.46

FILE 'MEDLINE' ENTERED AT 11:39:56 ON 11 MAR 2005

FILE 'BIOSIS' ENTERED AT 11:39:56 ON 11 MAR 2005
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FILE 'WPIDS' ENTERED AT 11:39:56 ON 11 MAR 2005
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=> d scan l19

L19  470 ANSWERS  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   piggyBac-mediated germline transformation in the beetle
     Tribolium castaneum.
IT   Methods & Equipment
        cloning: genetic techniques, laboratory techniques; genetic mapping:
        genetic techniques, laboratory techniques; sequencing: genetic
        techniques, laboratory techniques
IT   Miscellaneous Descriptors
        germline transformation

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):2
```

L19 470 ANSWERS BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Molecular cloning, sequencing and expression in Escherichia coli of the poly(3-hydroxyalkanoate) synthesis genes from Alcaligenes latus DSM1124.
IT Sequence Data
U47026: Genbank, nucleotide sequence

L19 470 ANSWERS BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Stable **transformation** of Trypanosoma brucei.
IT Sequence Data
amino acid sequence; molecular sequence data; nucleotide sequence; L03777: Genbank; L03778: Genbank
IT Miscellaneous Descriptors
BIFUNCTIONAL KINASE SIMILARITY; CLONING; NRKA GENE; NRKB GENE; PROTEIN SERINE-THREONINE KINASE SIMILARITY

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):2

L19 470 ANSWERS BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI HETERO DUPLEX ANALYSIS OF THE SEQUENCE RELATIONSHIPS BETWEEN THE GENOMES OF KIRSTEN AND HARVEY SARCOMA VIRUSES THEIR RESPECTIVE PARENTAL MURINE LEUKEMIA VIRUSES AND THE RAT ENDOGENOUS 30S RNA.
IT Miscellaneous Descriptors
ONCORNAVIRUS

L19 470 ANSWERS CAPLUS COPYRIGHT 2005 ACS on STN
CC 6-1 (General Biochemistry)
Section cross-reference(s): 10
TI Analysis of the nucleocapsid protein gene from Tomato spotted wilt virus as target and inducer for posttranscriptional gene silencing
ST nucleocapsid protein gene tomato spotted wilt virus posttranscriptional silencing; posttranscriptional gene silencing TSWV gene N expression
IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(N; anal. of nucleocapsid protein gene from tomato spotted wilt virus as target and inducer for posttranscriptional gene silencing)
IT Tomato spotted wilt virus
(TSWV; anal. of nucleocapsid protein gene from tomato spotted wilt virus as target and inducer for posttranscriptional gene silencing)
IT Disease resistance, plant
(anal. of nucleocapsid protein gene from tomato spotted wilt virus as target and inducer for posttranscriptional gene silencing)
IT Post-transcriptional processing
(gene silencing, VIGS (virus-induced gene silencing); anal. of nucleocapsid protein gene from tomato spotted wilt virus as target and inducer for posttranscriptional gene silencing)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(nucleocapsid, gene N; anal. of nucleocapsid protein gene from tomato spotted wilt virus as target and inducer for posttranscriptional gene silencing)

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):2

L19 470 ANSWERS CAPLUS COPYRIGHT 2005 ACS on STN
IC ICM C12N015-67
ICS C12N015-85; C12N015-63; C12Q001-68; C12N015-10; C12N015-62; G01N033-50
CC 3-1 (Biochemical Genetics)
TI Non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ

ST gene activation nontargeted recombination vector

IT Bone morphogenetic proteins
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(2; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Bone morphogenetic proteins
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(7; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Proteins, specific or class
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(A, hapten conjugated to nucleic acid primer; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Genetic vectors
(BAC and PAC; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Proteins, specific or class
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(G, hapten conjugated to nucleic acid primer; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Transferrins
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(apo-, hapten conjugated to nucleic acid primer; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Receptors
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(cell surface; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT YAC (yeast artificial chromosome)
(cloning vector; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(cytoskeleton-associated; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Proteins, specific or class
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(endotoxin-neutralizing, hapten conjugated to nucleic acid primer; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Genetic element
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(exon; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Proteins, specific or class
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(extracellular matrix-associated, hapten conjugated to nucleic acid primer; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Ankyrins
Antibodies
Antigens
Avidins
Cytokine receptors
Cytokines
Enzymes, biological studies
Fibrinogens
Immunoglobulin receptors
Insulin receptors
Integrins
Lipopolysaccharides
Spectrins
Transferrin receptors
Transferrins
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(hapten conjugated to nucleic acid primer; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Primers (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(hapten-conjugated; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Amphibian (Amphibia)
Animal cell
Annelid (Annelida)
Bird (Aves)
Fish
Fungi
Insect (Insecta)
Plant cell
Reptile
Yeast
(host; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(immediate early, cytomegalovirus, vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Ionizing radiation
(improved frequency and randomness of DNA integration; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Complement
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(inhibitor; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Codons
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(initiation, vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Antigens
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(large T, promoter for, vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Animal cell
(mammalian, host; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Cosmids
Drug screening
Genetic vectors
Molecular cloning
Plasmid vectors
Virus vectors
(non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT CD antigens
Hepatocyte growth factor
Interleukin 10
Interleukin 11
Interleukin 12
Interleukin 13
Interleukin 14
Interleukin 2
Interleukin 3
Interleukin 4
Interleukin 6
Interleukin 8
Ion channel
Lactoferrins
Leukemia inhibitory factor
Lipoprotein receptors
Platelet-derived growth factors
Stem cell factor
Thrombomodulin
Tumor necrosis factors
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Gene
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Multidrug resistance
(selectable marker encoded by vector; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Chimeric gene
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(selectable marker; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Genetic markers
(selectable; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(signal sequence, vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(splice donor, vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(transmembrane; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Recombination, genetic
(transposition, signal for, vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Human herpesvirus 4
Simian virus 40
(vector construct containing origin of replication of; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Interferons
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(α; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Actins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(β-, promoter for, vector containing; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT **Transforming** growth factors
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(β-; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Interferons
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(β; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT Interferons
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(γ; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)
IT 9000-94-6P, Antithrombin III 9001-24-5P, Blood-coagulation factor V 9001-25-6P, Blood-coagulation factor VII 9001-27-8P, Blood-coagulation factor VIII 9001-28-9P, Blood-coagulation factor IX 9001-29-0P, Blood-coagulation factor X 9001-42-7P, α-Glucosidase 9002-61-3P, Chorionic gonadotrophin 9002-64-6P, Parathyroid hormone 9002-68-0P, Follicle stimulating hormone 9002-72-6P, Growth hormone 9004-10-8P, Insulin, preparation 9007-92-5P, Glucagon, preparation 9014-42-0P, Thrombopoietin 9039-53-6P, Urokinase 9041-92-3P, α1-Antitrypsin 9061-61-4P, Nerve growth factor 11096-26-7P, Erythropoietin 37228-64-1P, Glucocerebrosidase 60202-16-6P, Protein C 61912-98-9P, Insulin-like growth factor 62031-54-3P, Fibroblast growth factor 62229-50-9P, Epidermal growth factor 81627-83-0P, Macrophage colony-stimulating factor 83869-56-1P, GM-CSF 106096-92-8P 118549-37-4P, Insulinotrophin 130939-66-1P, Neurotrophin-3 139639-23-9P, Tissue plasminogen activator 141436-78-4P, Protein kinase C 143011-72-7P, Granulocyte-colony stimulating factor 148348-15-6P, Fibroblast growth factor 7
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP

(Preparation)
(non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT 58-85-5D, Biotin, hapten conjugated to nucleic acid primer 1404-26-8D, Polymyxin B, hapten conjugated to nucleic acid primer 1672-46-4D, Digoxigenin, hapten conjugated to nucleic acid primer 9004-10-8D, Insulin, hapten conjugated to nucleic acid primer, biological studies 9013-20-1D, Streptavidin, hapten conjugated to nucleic acid primer 80804-53-1D, Complement C3bi, hapten conjugated to nucleic acid primer
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT 57-88-5P, Cholesterol, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(receptors; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

IT 9002-03-3, Dihydrofolate reductase 9002-06-6, Thymidine kinase 9012-49-1, Aspartate transcarbamylase 9016-12-0, Hypoxanthine phosphoribosyltransferase 9023-70-5, Glutamine synthetase 9024-93-5, Dihydroorotase 9026-23-7, Carbamyl phosphate synthase 9026-93-1, Adenosine deaminase 9028-27-7, Histidinol dehydrogenase 37350-22-4, Xanthine-guanine phosphoribosyltransferase 62213-36-9, Neomycin phosphotransferase 87110-39-2, Puromycin acetyltransferase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(selectable marker encoded by vector; non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ)

L19 470 ANSWERS CAPLUS COPYRIGHT 2005 ACS on STN
CC 11-0 (Plant Biochemistry)
Section cross-reference(s): 3
TI Expression of polygalacturonase and pectinesterase in normal and transgenic tomatoes
ST review polygalacturonase pectinesterase tomato
IT Tomato
Transformation, genetic
(expression of polygalacturonase and pectinesterase in normal and transgenic tomatoes)

IT 9025-98-3P, Pectinesterase 9032-75-1P, Polygalacturonase
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(expression of polygalacturonase and pectinesterase in normal and transgenic tomatoes)

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):2

L19 470 ANSWERS CAPLUS COPYRIGHT 2005 ACS on STN
CC 3-4 (Biochemical Genetics)
TI Expression of the penDE gene of Penicillium chrysogenum encoding isopenicillin N acyltransferase in Cephalosporium acremonium: production of benzylpenicillin by the **transformants**
ST Penicillium gene penDE Cephalosporium **transformation** benzylpenicillin
IT Cephalosporium acremonium
(benzylpenicillin formation by, subsequent to **transformation** with gene penDE of Penicillium chrysogenumium)

IT Penicillium chrysogenum
(isopenicillin N acyltransferase gene penDE of, Cephalosporium

acremonium **transformation** with, benzylpenicillin formation subsequent to)

IT Recombination, genetic
(**non-homologous**, of isopenicillin N acyltransferase gene penDE of Penicillium chrysogenum in Cephalosporium acremonium, after **transformation**)

IT Complementation, genetic
(of isopenicillin N synthase deficiency of Cephalosporium acremonium mutant, with Penicillium chrysogenumium gene cluster pcbC-penDE)

IT **Transformation**, genetic
(of Cephalosporium acremonium mutant, with Penicillium chrysogenumium gene cluster pcbC-penDE, benzylpenicillin formation subsequent to)

IT Ribonucleic acid formation
(messenger, benzylpenicillin-specifying, in Cephalosporium acremonium **transformed** with isopenicillin N acyltransferase gene penDE of Penicillium chrysogenum)

IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(penDE, for isopenicillin N acyltransferase, of Penicillium chrysogenum, Cephalosporium acremonium **transformation** with, benzylpenicillin formation subsequent to)

IT 78642-31-6
RL: PRP (Properties)
(deficiency in, of Cephalosporium acremonium mutant, Penicillium chrysogenumium gene cluster pcbC-penDE complementation of)

IT 11111-12-9, Cephalosporin
RL: PRP (Properties)
(formation of penicillin and, by Cephalosporium acremonium **transformed** with gene penDE of Penicillium chrysogenumium)

IT 61-33-6, Benzylpenicillin, biological studies
RL: FORM (Formation, nonpreparative)
(formation of, by Cephalosporium acremonium **transformed** with gene penDE of Penicillium chrysogenumium)

IT 54576-90-8
RL: PRP (Properties)
(gene penDE for, of Penicillium chrysogenum, Cephalosporium acremonium **transformation** with, benzylpenicillin formation subsequent to)

L19 470 ANSWERS WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

AN 2003-897579 [82] WPIDS
TI New CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A gene, useful for discriminating members of a gene family.

HOW MANY MORE ANSWERS DO YOU WISH TO SCAN? (1):end

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

L1 0 INITIAT? (W) DNA (W) UPTAKE
L2 373 INITIAT? (S) DNA (S) UPTAKE
L3 4746 NON (W) HOMOLOGOUS
L4 0 L2 AND L3
L5 209 STUFFER AND DNA
L6 0 L5 AND L2
L7 2254 DNA (W) UPTAKE
L8 1 L7 AND L3
L9 0 L5 AND L7

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L10        18629 DNA (S) UPTAKE
L11            0 L10 AND L5
L12            7 L10 AND L3
L13            4 DUP REM L12 (3 DUPLICATES REMOVED)
                 E DIAZ (W) TORRES MARIA/AU
                 E DIAZ TORRES MARIA/AU
L14           54 E1-E4
L15           23 DUP REM L14 (31 DUPLICATES REMOVED)
L16            2 TRANSFORM? AND L15
L17            0 L3 AND L5
L18      1447160 TRANSFORM?
L19          470 L3 AND L18
L20            0 L19 AND L5
L21            5 L19 AND L10
L22            2 DUP REM L21 (3 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:39:56 ON 11
     MAR 2005

=> construct and l19
L23           33 CONSTRUCT AND L19

=> dup rem l23
PROCESSING COMPLETED FOR L23
L24           19 DUP REM L23 (14 DUPLICATES REMOVED)

=> t ti l24 1-19

L24  ANSWER 1 OF 19  EMBASE  COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
     on STN
TI   A rapid method for promoter exchange in Aspergillus nidulans using
     recombinant PCR.

L24  ANSWER 2 OF 19  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Efficient generation of stable expression cell lines through the use of
     scorable homeostatic reporter genes for production of protein complexes

L24  ANSWER 3 OF 19  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   New nucleic acid fragment encoding a PAIGB polypeptide, useful in
     preparing a composition for diagnosing, treating or preventing bone
     related disorders, e.g., osteoporosis.

L24  ANSWER 4 OF 19     MEDLINE on STN                    DUPLICATE 1
TI   Efficient gene targeting in Kluyveromyces lactis.

L24  ANSWER 5 OF 19  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   Generating genetically modified vertebrate precursor lymphocytes for
     producing any heterologous antibody or binding protein comprises effecting
     differentiation of the precursor lymphocytes into mature lymphoid lineage
     cells.

L24  ANSWER 6 OF 19  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Human gene targeting by adeno-associated virus vectors is enhanced by DNA
     double-strand breaks

L24  ANSWER 7 OF 19  EMBASE  COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
     on STN
TI   Expression of the Kappa (K) Light Chain of Mouse Anticreatine Kinase-M
     (MAK33) Antibody in the Yeast Hansenula polymorpha.
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L24 ANSWER 8 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.

L24 ANSWER 9 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN
TI Non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ

L24 ANSWER 10 OF 19 MEDLINE on STN DUPLICATE 2
TI The restoration of fertility in male sterile tobacco demonstrates that transgene silencing can be mediated by T-DNA that has no DNA homology to the silenced transgene.

L24 ANSWER 11 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
TI Expression of endogenous genes by **non-homologous** recombination of a vector **construct** with cellular DNA

L24 ANSWER 12 OF 19 MEDLINE on STN DUPLICATE 4
TI Homologous **transformation** of Trichoderma hamatum with an endochitinase encoding gene, resulting in increased levels of chitinase activity.

L24 ANSWER 13 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN
TI Down regulation of two **non-homologous** endogenous genes with a single chimeric gene **construct**

L24 ANSWER 14 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Slow-growing mycobacteria **transformed** with heterologous DNA - useful as vaccines in which the mycobacteria stimulate long-term memory or immunity.

L24 ANSWER 15 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN
TI Genetic **construct** for selection of homologous recombinants on a single selective medium

L24 ANSWER 16 OF 19 MEDLINE on STN DUPLICATE 5
TI Stable **transformation** of Trypanosoma brucei.

L24 ANSWER 17 OF 19 MEDLINE on STN DUPLICATE 6
TI Down-regulation of two **non-homologous** endogenous tomato genes with a single chimaeric sense gene **construct**.

L24 ANSWER 18 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Genomic modification using DNA targetting for treating genetic disorder etc. - by using vector containing DNA with homology but different to a target locus and a marker gene.

L24 ANSWER 19 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN
TI Targeted disruption of a human interferon-inducible gene detected by secretion of human growth hormone

=> d ibib abs l24 1-19

L24 ANSWER 1 OF 19 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2004532589 EMBASE
TITLE: A rapid method for promoter exchange in Aspergillus nidulans using recombinant PCR.
AUTHOR: Zarrin M.; Leeder A.C.; Turner G.
CORPORATE SOURCE: . g.turner@sheffield.ac.uk

SOURCE: Fungal Genetics and Biology, (2005) 42/1 (1-8).
Refs: 25
ISSN: 1087-1845 CODEN: FGBIFV
PUBLISHER IDENT.: S 1087-1845(04)00156-2
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Recombinant PCR has been used to generate linear fragments for promoter replacement by **transformation** in Aspergillus nidulans. A cassette vector carrying the pyr-4 **non-homologous** selectable marker and conditional promoter Pr-alcA was constructed for use as a template for PCR, and is suitable for testing the function of essential genes. Two genes involved in polar growth, cotA and bemA, were used to assess the system. Efficient targeting was possible with both genes using approximately 500 bp of flanking homologous sequence. Depending on yield, the linear PCR product could be used directly for **transformation**, or after first cloning into a suitable vector. bemA, a putative homologue of the Saccharomyces cerevisiae BEM1 gene was identified through sequence comparison. In A. nidulans, this protein appears to have a similar role to the yeast Bem1p, which acts as a scaffold protein involved in the establishment of cell polarity. .COPYRGT. 2004 Elsevier Inc. All rights reserved.

L24 ANSWER 2 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:292111 CAPLUS
DOCUMENT NUMBER: 140:298627
TITLE: Efficient generation of stable expression cell lines through the use of scorable homeostatic reporter genes for production of protein complexes
INVENTOR(S): Dubridge, Robert B.
PATENT ASSIGNEE(S): Protein Design Labs, Inc., USA
SOURCE: PCT Int. Appl., 90 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004029284	A2	20040408	WO 2003-US31311	20030930
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004115814	A1	20040617	US 2003-676476	20030930
PRIORITY APPLN. INFO.:			US 2002-415216P P	20020930

AB The present invention provides compns., systems and methods for identifying and utilizing advantageous genomic sites for expression of recombinant proteins. This is accomplished by randomly inserting plastic expression systems that permit exchange of their coding regions while leaving the remainder of the expression system, including the promoter, in place. More specifically, the invention described herein provides integration cassettes that are inserted into cellular genetic material by

a **non-homologous** recombination event. These integration cassettes comprise expression systems for selectable and scorable reporter genes that allow cells successfully **transformed** with the integration cassettes to be identified and the level of expression supported by the cassette at its site of insertion to be established. The methods and vectors for site-specific recombination in a cell of the present invention can be used to obtain persistent gene expression in a cell and to modulate gene expression. One preferred method according to the invention comprises contacting a cell with a vector comprising an origin of replication functional in mammalian cells located between first and second recombining sites located in parallel. Another preferred method comprises, in part, contacting a cell with a vector comprising first and second recombining sites in antiparallel orientations such that the vector is internalized by the cell. In both methods, the cell is further provided with a site-specific recombinase that effects recombination between the first and second recombining sites of the vector. The **transformation** of CHO cells using CJA8 exchangeable reporter element and scorable reporter gene, CD4, was performed. The exchanging a reporter segment for a target segment using Flp recombination system was demonstrated. The construction of an antibody library was demonstrated.

L24 ANSWER 3 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-420299 [39] WPIDS
DOC. NO. CPI: C2004-157851
TITLE: New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.
DERWENT CLASS: B04 D16
INVENTOR(S): BABIJ, P; MURRILLS, R J; ROBINSON, J A; STOJANOVIC-SUSULIC, V
PATENT ASSIGNEE(S): (AMHP) WYETH
COUNTRY COUNT: 107
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004044152	A2	20040527	(200439)*	EN	169
RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
US 2004146906	A1	20040729	(200450)		
AU 2003294250	A1	20040603	(200470)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004044152	A2	WO 2003-US35655	20031110
US 2004146906	A1 Provisional	US 2002-425532P	20021112
		US 2003-705716	20031110
AU 2003294250	A1	AU 2003-294250	20031110

FILING DETAILS:

PATENT NO	KIND	PATENT NO

AU 2003294250 A1 Based on WO 2004044152

PRIORITY APPLN. INFO: US 2002-425532P 20021112; US 2003-705716 20031110

AN 2004-420299 [39] WPIDS

AB WO2004044152 A UPAB: 20040621

NOVELTY - A new isolated nucleic acid fragment encoding a PAIGB polypeptide comprises:

(1) a fragment encoding a protein comprising a sequence not given in the specification;

(2) a fragment encoding an amino acid sequence having at least 85% identity with the protein;

(3) a fragment that hybridizes with (1) under hybridization conditions of 6 multiply SSC (1M NaCl), 45-50% formamide, 1% SDS at 37 deg. C and a wash in 0.5 multiply to 1 multiply SSC at 55-60 deg. C; or

(4) a complement of (1), (2) or (3).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) a polypeptide encoded by the isolated nucleic acid fragment;

(2) a chimeric **construct** comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences;

(3) a host cell **transformed** with the chimeric **construct**;

(4) a vector comprising the nucleic acid fragment;

(5) obtaining a nucleic acid fragment encoding the polypeptide;

(6) obtaining a polypeptide;

(7) detecting the presence of the nucleic acid fragment;

(8) an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide;

(9) a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody;

(10) an agent that alters the expression of PAIGB gene or polypeptide;

(11) determining whether an agent alters the expression of PAIGB mRNA;

(12) screening agents for effectiveness in altering expression of the nucleic acid fragment;

(13) screening for agents useful for treating bone related disorders;

(14) evaluating the efficacy of a treatment of a bone related disorder in a subject;

(15) identifying polypeptides capable of binding to PAIGB;

(16) monitoring the effectiveness of treatment of a subject with a bone related agent;

(17) a transgenic animal comprising the DNA;

(18) an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals;

(19) studying bone mass determinants;

(20) studying the modulation of bone mass;

(21) studying an effect of PAIGB on bone disorders;

(22) identifying an agent for treating bone related disorders;

(23) identifying whether an agent which has bone forming activity; and

(24) a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced.

ACTIVITY - Osteopathic. No biological data given.

MECHANISM OF ACTION - Gene therapy.

USE - The nucleic acid is useful in preparing a composition for

diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.
Dwg.0/1

L24 ANSWER 4 OF 19 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2004379475 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15282801
TITLE: Efficient gene targeting in Kluyveromyces lactis.
AUTHOR: Kooistra Rolf; Hooykaas Paul J J; Steensma H Yde
CORPORATE SOURCE: Institute of Biology, Leiden University, Wassenaarseweg 64, 2333 AL Leiden, The Netherlands.
SOURCE: Yeast (Chichester, England), (2004 Jul 15) 21 (9) 781-92. Journal code: 8607637. ISSN: 0749-503X.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200409
ENTRY DATE: Entered STN: 20040730
Last Updated on STN: 20040921
Entered Medline: 20040917

AB Integration of a DNA fragment in a host genome requires the action of a double-strand break (DSB) repair mechanism. Homologous recombination (HR) is initiated by binding of Rad52p to DNA ends and results in targeted integration. Binding of the Ku heterodimer (Ku70p/Ku80p) results in random integration via **non-homologous** end joining (NHEJ). In contrast to Saccharomyces cerevisiae, the budding yeast Kluyveromyces lactis shows variable, but in general low, gene targeting efficiency. To study and to improve gene targeting efficiency, K. lactis has been used as a model. The KlRAD51, KlRAD52 and KlKU80 genes have been isolated and deletion mutants for these genes have been constructed. Efficiency of gene targeting was determined at the KlADE2 locus using targeting constructs with different lengths of homologous flanking sequences. In wild-type K. lactis, the gene targeting efficiency ranged from 0% with 50 to 88% with 600 bp flanks. The Klku80 mutant, however, showed >97% gene targeting efficiency independently of the size of the homologous flanks. These results demonstrate that deletion of the NHEJ mechanism results in a higher gene targeting efficiency. Furthermore, increased gene targeting efficiency was achieved by the **transformation** of wild-type K. lactis with the KlADE2 deletion **construct** in the presence of excess small DNA fragments. Using this method, PCR-generated deletion constructs containing only 50 bp of homologous flanking sequences resulted in efficient targeted gene replacement.

L24 ANSWER 5 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-571360 [54] WPIDS
DOC. NO. CPI: C2003-154442
TITLE: Generating genetically modified vertebrate precursor lymphocytes for producing any heterologous antibody or binding protein comprises effecting differentiation of the precursor lymphocytes into mature lymphoid lineage cells.
DERWENT CLASS: B04 D16
INVENTOR(S): GRAWUNDER, U; MELCHERS, G F
PATENT ASSIGNEE(S): (GRAW-I) GRAWUNDER U; (MELC-I) MELCHERS G F; (FOUR-N) 4-ANTIBODY AG; (FOUR-N) 4 ANTIBODY AG
COUNTRY COUNT: 101
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

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-------------------------------------------------
EP 1321477      A1 20030625 (200354)* EN  111
    R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
       RO SE SI TR
WO 2003068819   A1 20030821 (200356)# EN
   RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
       NL OA PT SD SE SL SZ TR TZ UG ZM ZW
    W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
       DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
       KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT
       RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2002226390   A1 20030904 (200428)#
EP 1321477      B1 20041013 (200467)  EN
    R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
       RO SE SI TR
DE 60106469     E  20041118 (200476)
```

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1321477	A1	EP 2001-130805	20011222
WO 2003068819	A1	WO 2001-EP15303	20011222
AU 2002226390	A1	WO 2001-EP15303	20011222
		AU 2002-226390	20011222
EP 1321477	B1	EP 2001-130805	20011222
DE 60106469	E	DE 2001-00106469	20011222
		EP 2001-130805	20011222

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002226390	A1 Based on	WO 2003068819
DE 60106469	E Based on	EP 1321477

PRIORITY APPLN. INFO: EP 2001-130805 20011222; WO
2001-EP15303 20011222; AU
2002-226390 20011222

AN 2003-571360 [54] WPIDS

AB EP 1321477 A UPAB: 20040826

NOVELTY - Generating vertebrate lymphocytes that can be used for the production of any heterologous antibody, antigen receptor, artificial binding protein, or their functional fragments, comprising:

(a) genetically modifying vertebrate precursor lymphocytes; and

(b) effecting differentiation of the precursor lymphocytes into mature lymphoid lineage cells either in vitro or in vivo, is new.

DETAILED DESCRIPTION - Generating vertebrate lymphocytes that can be used for the production of any heterologous antibody, antigen receptor, artificial binding protein, or their functional fragments, comprising:

(a) genetically modifying vertebrate precursor lymphocytes, which:

(a) are derived from primary lymphoid organs; and

(b) have the potential to differentiate into mature lymphoid lineage cells by introducing at least one exogenous genetic element encoding at least one heterologous antibody, antigen receptor, artificial binding protein, or their fragments; and

(b) effecting differentiation of the precursor lymphocytes into mature lymphoid lineage cells either in vitro or in vivo, thus, generating lymphocytes capable of producing the heterologous antibody, antigen receptor, artificial binding protein, or their fragments, is new.

INDEPENDENT CLAIMS are included for the following:

(1) genetically modified vertebrate precursor lymphocytes and more

mature lymphoid lineage cells derived from the precursor lymphocytes, obtained by the method;

(2) immortalized cells producing heterologous antibodies, antigen receptor, artificial binding protein, or their fragments;

(3) vector or genetic constructs for carrying out the method; and

(4) a pharmaceutical or diagnostic preparation, comprising at least one antibody, antigen receptor, artificial binding protein, or their fragments, obtained by the method, displaying either wild-type immune effector functions, or modified or artificial effector functions not derivable from germline encoded heterologous immunoglobulins or antigen receptors.

USE - The method and the genetically modified and differentiated vertebrate lymphocytes are useful in the production of any heterologous antibody, artificial binding protein, antigen receptor, or their fragments, where the antibody is monoclonal or polyclonal, or partially resembles a human antibody, binding protein or antigen receptor (claimed). The antibodies are useful for the diagnosis, prevention and treatment of diseases.

ADVANTAGE - The method combines the advantages of both the phage display system (i.e. speed and flexibility in generating human antibodies, and the ability to modify and improve the properties of existing antibodies), and of the human immunoglobulin transgenic mouse technology (i.e. the ability to obtain high affinity antibodies due to affinity maturation occurring in the immune system, and the production antibodies with physiologic and natural structural features).

Dwg.0/15

L24 ANSWER 6 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:368243 CAPLUS

DOCUMENT NUMBER: 139:64044

TITLE: Human gene targeting by adeno-associated virus vectors is enhanced by DNA double-strand breaks

AUTHOR(S): Miller, Daniel G.; Petek, Lisa M.; Russell, David W.

CORPORATE SOURCE: Division of Medical Genetics, University of Washington, Seattle, WA, 98195, USA

SOURCE: Molecular and Cellular Biology (2003), 23(10), 3550-3557

CODEN: MCEBD4; ISSN: 0270-7306

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The use of adeno-associated virus (AAV) to package gene-targeting vectors as single-stranded linear mols. has led to significant improvements in mammalian gene-targeting frequencies. However, the mol. basis for the high targeting frequencies obtained is poorly understood, and there could be important mechanistic differences between AAV-mediated gene targeting and conventional gene targeting with transfected double-stranded DNA constructs. Conventional gene targeting is thought to occur by the double-strand break (DSB) model of homologous recombination, as this can explain the higher targeting frequencies observed when DSBs are present in the targeting **construct** or target locus. Here we compare AAV-mediated gene-targeting frequencies in the presence and absence of induced target site DSBs. Retroviral vectors were used to introduce a mutant lacZ gene containing an I-SceI cleavage site and to efficiently deliver the I-SceI endonuclease, allowing us to carry out these studies with normal and **transformed** human cells. Creation of DSBs by I-SceI increased AAV-mediated gene-targeting frequencies 60- to 100-fold and resulted in a precise correction of the mutant lacZ reporter gene. These expts. demonstrate that AAV-mediated gene targeting can result in repair of a DNA DSB and that this form of gene targeting exhibits fundamental similarities to conventional gene targeting. In addition, our findings suggest that the selective creation of DSBs by using viral delivery

systems can increase gene-targeting frequencies in scientific and therapeutic applications.
REFERENCE COUNT: 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L24 ANSWER 7 OF 19 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2004192663 EMBASE
TITLE: Expression of the Kappa (K) Light Chain of Mouse Anticreatine Kinase-M (MAK33) Antibody in the Yeast Hansenula polymorpha.
AUTHOR: Abdel-Salam H.A.; Enan G.; Serry F.M.E.; Ghonaim M.; Abdel-Latif H.K.; Hollenberg C.P.
CORPORATE SOURCE: Egypt
SOURCE: Chinese Pharmaceutical Journal, (2003) 55/3 (197-206). Refs: 43
ISSN: 1016-1015 CODEN: CYHCEX
COUNTRY: Taiwan,Province of China
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB An expression plasmid was constructed and **transformed** to the methylotrophic yeast Hansenulapolymorpha to produce the kappa chain peptide of IgG antibody (MAK33). Hansenula polymorpha appears to be one of the most efficient host cells for the expression of genetically engineered antibody genes. Although the rate of **transformation** of this yeast by polyethylene glycol was low (3-5 cells/1.0 μg plasmid DNA), yet the **transformants** showed high mitotic stability for more than 100 generations. The expression plasmid was integrated within the yeast genome at one or more integrations site (s) with low and multicopy-number plasmids via a **non-homologous** integration mechanism. An N-terminal glucoamylase gene fragment was linked to the light chain (kappa) gene of the F(ab) derivative of the MAK33 antibody. Prepro-alpha factor of the yeast Saccharomyces cerevisiae was inserted into the plasmid between the glucoamylase and light chain genes as a secretion signal sequence for the light chain peptide. The kappa chain was produced at 50 mg/L free protein in the culture medium and 500 mg/L entrapped within the cells, amounting to 550 mg/L and representing about 10% of the total cell protein. The prepro-α factor was shown to be incompletely processed in Hansenula polymorpha and the pro-segment accompanied the light chain peptide.

L24 ANSWER 8 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-095652 [09] WPIDS
DOC. NO. NON-CPI: N2003-075841
DOC. NO. CPI: C2003-024324
TITLE: Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): JONES, A E; MICHAEL, N P; STUBBS, S L J; THOMAS, N
PATENT ASSIGNEE(S): (AMSH) AMERSHAM BIOSCIENCES UK LTD; (AMSH) AMERSHAM PHARMACIA BIOTECH UK LTD; (JONE-I) JONES A E; (MICH-I) MICHAEL N P; (STUB-I) STUBBS S L J; (THOM-I) THOMAS N
COUNTRY COUNT: 98
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
GB 2374868	A	20021030	(200309)*		52

WO 2002085936 A1 20021031 (200309) EN
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
GB 2374868 B 20030709 (200353)
US 2003175859 A1 20030918 (200362)
EP 1381625 A1 20040121 (200410) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
AU 2001292040 A1 20021105 (200433)
US 2004138420 A1 20040715 (200447)
EP 1381625 B1 20041124 (200477) EN
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TR
DE 60107471 E 20041230 (200502)
JP 2005502323 W 20050127 (200510) 77

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
GB 2374868	A	GB 2001-23288	20010928
WO 2002085936	A1	WO 2001-GB4363	20010928
GB 2374868	B	GB 2001-23288	20010928
US 2003175859	A1	US 2001-967301	20010928
EP 1381625	A1	EP 2001-972260	20010928
		WO 2001-GB4363	20010928
AU 2001292040	A1	AU 2001-292040	20010928
US 2004138420	A1 Div ex	US 2001-967301	20010928
		US 2004-757624	20040114
EP 1381625	B1	EP 2001-972260	20010928
		WO 2001-GB4363	20010928
DE 60107471	E	DE 2001-00107471	20010928
		EP 2001-972260	20010928
		WO 2001-GB4363	20010928
JP 2005502323	W	WO 2001-GB4363	20010928
		JP 2002-583462	20010928

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 1381625	A1	Based on	WO 2002085936
AU 2001292040	A1	Based on	WO 2002085936
EP 1381625	B1	Based on	WO 2002085936
DE 60107471	E	Based on	EP 1381625
		Based on	WO 2002085936
JP 2005502323	W	Based on	WO 2002085936

PRIORITY APPLN. INFO: GB 2001-9858 20010423
AN 2003-095652 [09] WPIDS
AB GB 2374868 A UPAB: 20030206
NOVELTY - A fluorescent protein (I) derived from green fluorescent protein (GFP) or any functional GFP analog, has an amino acid sequence which is modified by amino acid substitution at position F64, at position S65 or E222, and at position S175 compared with the amino acid sequence of wild-type GFP, and has different excitation spectrum and/or emission spectrum compared with wild-type GFP, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a fusion compound (II) comprising a protein of interest fused to (I);

(2) a nucleic acid molecule (III) comprising a nucleotide sequence encoding (I) or (II);

(3) an expression vector (IV) comprising suitable expression control sequences operably linked to (III); and

(4) a host cell (V) **transformed** or transfected with a DNA **construct** comprising (IV).

USE - (III) is useful for measuring the expression of a protein of interest in a cell, by introducing (III) into a cell, where (III) is operably linked to and under the control of an expression control sequence which moderates expression of the protein of interest, culturing the cell under conditions suitable for the expression of the protein of interest, and detecting the fluorescence emission of GFP or functional GFP analog. (III) is useful for determining the cellular and/or extracellular localization of a protein of interest. (III) is also useful for comparing the effect of one or more test substance(s) on the expression and/or localization of one or more different protein(s) of interest in a cell. The method involves:

(a) introducing into a cell, (III) operably linked to and under the control of a first expression control sequence and optionally fused to a nucleotide sequence encoding a fusion protein of interest, and optionally, at least one different nucleic acid molecule encoding a protein reporter molecule fused to a different protein of interest, where the nucleic acid molecule is operably linked to and under the control of a second expression control sequence, and the protein reporter molecule has or is capable of generating an emission signal which is spectrally distinct from that of GFP or functional GFP analog;

(b) culturing the cells under conditions suitable for the expression of the protein(s) of interest in the presence and absence of the test substance(s);

(c) determining the expression and/or localization of the protein(s) in the cells by detecting the fluorescence emission by optical means; and

(d) comparing the fluorescence emission obtained in the presence and absence of the test substance(s).

The samples of the cells in a fluid medium are introduced into separate vessels for each of the test substances to be studied (not claimed).

(I) is useful as a non-toxic marker for selection of transfected cells, as a protein label in living and fixed cells, as a marker in cell or organelle fusion, for visualizing translocation of intracellular proteins to a specific organelle, as a secretion marker, as genetic reporter or protein tag for protein and gene expression in transgenic animals, as a cell or organelle integrity marker, as a transfection marker, as a marker to be used in combination with fluorescent activated cell sorting (FACS), as real-time probe working at near physiological concentrations, for performing transposon vector mutagenesis, and as a reporter for bacterial detection.

ADVANTAGE - (I) exhibits enhanced fluorescence relative to wild type GFP, when expressed in **non-homologous** cells at temperatures above 30 deg. C, and excited at 490 nm. (I) detects GFP reporters in mammalian cells at lower levels of expression with increased sensitivity relative to wild type GFP.

Dwg.0/7

L24 ANSWER 9 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:592846 CAPLUS

DOCUMENT NUMBER: 133:173007

TITLE: Non-targeted activation of endogenous gene expression or over-expression by recombination methods in situ

INVENTOR(S): Harrington, John J.; Sherf, Bruce; Rundlett, Stephen

PATENT ASSIGNEE(S): Athersys, Inc., USA

SOURCE: PCT Int. Appl., 241 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000049162	A2	20000824	WO 2000-US4429	20000222
WO 2000049162	A3	20001228		
W: AE, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6602686	B1	20030805	US 1999-455659	19991207
US 6410266	B1	20020625	US 2000-479122	20000107
US 6670185	B1	20031230	US 2000-479123	20000107
US 6361972	B1	20020326	US 2000-481375	20000110
US 6541221	B1	20030401	US 2000-481282	20000111
US 6524824	B1	20030225	US 2000-481355	20000112
US 6524818	B1	20030225	US 2000-484997	20000118
US 6623958	B1	20030923	US 2000-484996	20000118
US 6740503	B1	20040525	US 2000-484317	20000118
CA 2364267	AA	20000824	CA 2000-2364267	20000222
EP 1155131	A2	20011121	EP 2000-908750	20000222
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
BR 2000008313	A	20030923	BR 2000-8313	20000222
JP 2004501601	T2	20040122	JP 2000-599886	20000222
US 2004162416	A1	20040819	US 2001-760897	20010117
ZA 2001006777	A	20030514	ZA 2001-6777	20010817
US 2003180267	A1	20030925	US 2002-331329	20021230

PRIORITY APPLN. INFO.:		
US 1999-253022	A	19990219
US 1999-263814	A	19990308
US 1999-276820	A	19990326
US 1997-941223	B2	19970926
US 1998-159643	B2	19980924
WO 2000-US4429	W	20000222
US 2000-515124	B1	20000227

AB The present invention is directed generally to activating gene expression or causing over-expression of a gene by recombination methods in situ. The invention also is directed generally to methods for expressing an endogenous gene in a cell at levels higher than those normally found in the cell. In one embodiment of the invention, expression of an endogenous gene is activated or increased following integration into the cell, by **non-homologous** or illegitimate recombination, of a regulatory sequence that activates expression of the gene. In another embodiment, the expression of the endogenous gene may be further increased by co-integration of one or more amplifiable markers, and selecting for increased copies of the one or more amplifiable markers located on the integrated vector. In another embodiment, the invention is directed to activation of endogenous genes by non-targeted integration of specialized activation vectors, which are provided by the invention, into the genome of a host cell. The invention also provides methods for the identification, activation, isolation, and/or expression of genes undiscoverable by current methods since no target sequence is necessary

for integration. The invention also provides methods for isolation of nucleic acid mols. (particularly cDNA mols.) encoding a variety of proteins, including transmembrane proteins, and for isolation of cells expressing such transmembrane proteins which may be heterologous transmembrane proteins. The invention also is directed to isolated genes, gene products, nucleic acid mols., to compns. comprising such genes, gene products and nucleic acid mols., and to vectors and host cells comprising such genes and nucleic acid mols., that may be used in a variety of therapeutic and diagnostic applications. Thus, by the present invention, endogenous genes, including those associated with human disease and development, may be activated and isolated without prior knowledge of the sequence, structure, function, or expression profile of the genes.

L24 ANSWER 10 OF 19 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2001089905 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10951693
TITLE: The restoration of fertility in male sterile tobacco demonstrates that transgene silencing can be mediated by T-DNA that has no DNA homology to the silenced transgene.
AUTHOR: Hird D L; Paul W; Hollyoak J S; Scott R J
CORPORATE SOURCE: Department of Biology, University of Leicester, UK.
SOURCE: Transgenic research, (2000 Apr) 9 (2) 91-102.
Journal code: 9209120. ISSN: 0962-8819.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010125

AB Male sterile tobacco plants expressing a pathogenesis-related (PR) beta-1,3-glucanase gene driven by the Arabidopsis thaliana A3 or A9 tapetum-specific promoter, were partially restored to fertility by retransformation with a range of pA9-driven sense and antisense PR glucanase fragments. The restored plants exhibited improved seed set. PR glucanase protein was undetectable in the anthers of these plants and there was an associated increase in microsporocyte callose, the structural target of the A3 and A9-driven PR glucanase. This phenotype was not solely dependent on interactions between sense and antisense PR glucanase transcripts since a pA9-driven restorer was also capable of down regulating a pA3-GUS **construct** in the absence of extensive promoter, coding region, or terminator sequence homology. Since the A3 and A9 promoters have similar temporal and spatial expression patterns, it is possible that trans-acting factors common to both promoters become limiting in the PR glucanase double **transformants** resulting in improved levels of fertility. An alternative hypothesis is that additional sequences present in both the silencing and target T-DNAs can mediate the silencing of adjacent **non-homologous** transgenes.

L24 ANSWER 11 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 1999:223034 CAPLUS
DOCUMENT NUMBER: 130:263127
TITLE: Expression of endogenous genes by **non-homologous** recombination of a vector **construct** with cellular DNA
INVENTOR(S): Harrington, John J.
PATENT ASSIGNEE(S): Athersys, Inc., USA
SOURCE: PCT Int. Appl., 109 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9915650	A1	19990401	WO 1998-US20094	19980925
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
ZA 9808795	A	19990329	ZA 1998-8795	19980925
CA 2304642	AA	19990401	CA 1998-2304642	19980925
AU 9895816	A1	19990412	AU 1998-95816	19980925
AU 750025	B2	20020711		
EP 1017803	A1	20000712	EP 1998-949508	19980925
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9812540	A	20011226	BR 1998-12540	19980925
NZ 504185	A	20030228	NZ 1998-504185	19980925
JP 2003535564	T2	20031202	JP 2000-512942	19980925
US 6602686	B1	20030805	US 1999-455659	19991207
US 6410266	B1	20020625	US 2000-479122	20000107
US 6670185	B1	20031230	US 2000-479123	20000107
US 6361972	B1	20020326	US 2000-481375	20000110
US 6541221	B1	20030401	US 2000-481282	20000111
US 6524824	B1	20030225	US 2000-481355	20000112
US 6524818	B1	20030225	US 2000-484997	20000118
US 6623958	B1	20030923	US 2000-484996	20000118
US 6740503	B1	20040525	US 2000-484317	20000118
NO 2000001497	A	20000525	NO 2000-1497	20000322
US 2004162416	A1	20040819	US 2001-760897	20010117
US 2003180267	A1	20030925	US 2002-331329	20021230

PRIORITY APPLN. INFO.:		
US 1997-941223	A	19970926
US 1998-159643	A	19980924
WO 1998-US20094	W	19980925
US 1999-253022	B2	19990219
US 1999-263814	B2	19990308
US 1999-276820	A3	19990326
US 2000-515124	B1	20000227

AB The present invention relates generally to activating gene expression or causing over-expression of a gene by recombination methods in situ. The invention also relates generally to methods for expressing an endogenous gene in a cell at levels higher than those normally found in the cell. In one embodiment of the invention, expression of an endogenous gene is activated or increased following integration into the cell, by **non-homologous** or illegitimate recombination, of a regulatory sequence that activates expression of the gene. In another embodiment, the expression of the endogenous gene may be further increased by co-integration of one or more amplifiable markers, and selecting for increased copies of the one or more amplifiable markers located on the integrated vector. The invention also provides methods for the identification and expression of genes undiscoverable by current methods since no target sequence is necessary for integration. The invention also provides methods for isolation of nucleic acid mols. (particularly cDNA mols.) encoding transmembrane proteins, and for isolation of cells expressing such transmembrane proteins which may be heterologous transmembrane proteins. The invention also relates to isolated genes,

gene products, nucleic acid mols., and compns. comprising such genes, gene products and nucleic acid mols., that may be used in a variety of therapeutic and diagnostic applications. Thus, by the present invention, endogenous genes, including those associated with human disease and development, may be activated and isolated without prior knowledge of the sequence, structure, function, or expression profile of the genes.
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L24 ANSWER 12 OF 19 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 1998415120 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9742695
TITLE: Homologous **transformation** of Trichoderma hamatum with an endochitinase encoding gene, resulting in increased levels of chitinase activity.
AUTHOR: Giczey G; Kerenyi Z; Dallmann G; Hornok L
CORPORATE SOURCE: Agricultural Biotechnology Center, Godollo, Hungary.
SOURCE: FEMS microbiology letters, (1998 Aug 15) 165 (2) 247-52. Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U88560
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981027
AB A 42-kDa endochitinase encoding gene, Tham-ch, was cloned by screening the genomic library of Trichoderma hamatum strain Tam-61 with a PCR-amplified chitinase sequence from the same fungus. Tham-ch with its own regulatory sequences was reintroduced into the host strain. The integration of the **transforming construct** was stable only in one copy. Homologous integration occurred in nine **transformants**, while **non-homologous** integration was detected in one **transformant**. All but one **transformant** expressed higher levels of chitinase activity in comparison to the wild-type recipient strain; the maximum level of increase was 5-fold. Duplicating the copy number of the highly conserved approximately 42-kDa endochitinase encoding gene appears to be one potential means by which the biocontrol capability of the Trichoderma species might be improved.

L24 ANSWER 13 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1996:637981 CAPLUS
DOCUMENT NUMBER: 125:294060
TITLE: Down regulation of two **non-homologous** endogenous genes with a single chimeric gene **construct**
AUTHOR(S): Jones, C. G.; Seymour, G. B.; Bird, C. R.; Schuch, W.; Boniwell, J.; Lycett, G. W.; Tucker, G. A.
CORPORATE SOURCE: School of Agricultural and Food Sciences, Univ. of Nottingham, Leics, LE12 5RD, UK
SOURCE: Mechanisms and Applications of Gene Silencing, [Easter School in Agricultural Science], 57th, Sutton Bonington, UK, Mar., 1995 (1996), Meeting Date 1995, 85-95. Editor(s): Grierson, Donald; Lycett, Grantley W.; Tucker, Gregory A. Nottingham University Press: Nottingham, UK.
CODEN: 63NBAT
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review with 23 refs. on the mol. biol. of polygalacturonase and

pectinesterase, and **transformation** of a chimeric gene for the 2 enzymes.

L24 ANSWER 14 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 1995-075243 [10] WPIDS
CROSS REFERENCE: 1988-271166 [38]; 1990-051704 [07]; 1991-022237 [03]; 1995-075244 [10]
DOC. NO. CPI: C1995-033503
TITLE: Slow-growing mycobacteria **transformed** with heterologous DNA - useful as vaccines in which the mycobacteria stimulate long-term memory or immunity.
DERWENT CLASS: B04 D16
INVENTOR(S): ALDOVINI, A; YOUNG, R A
PATENT ASSIGNEE(S): (WHED) WHITEHEAD INST BIOMEDICAL RES
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9503417	A2	19950202	(199510)*	EN	59
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE					
W: CA JP					
WO 9503417	A3	19950406	(199614)		
EP 710287	A1	19960508	(199623)	EN	
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE					
US 5866403	A	19990202	(199912)		
US 6022745	A	20000208	(200014)		
US 6355486	B1	20020312	(200221)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9503417	A2		WO 1994-US8267	19940722
WO 9503417	A3		WO 1994-US8267	19940722
EP 710287	A1		EP 1994-922679	19940722
			WO 1994-US8267	19940722
US 5866403	A	CIP of	US 1987-20451	19870302
		CIP of	US 1988-163546	19880303
		CIP of	US 1988-216390	19880614
		CIP of	US 1988-223089	19880722
		CIP of	US 1989-361944	19890605
		CIP of	US 1989-367894	19890619
		Cont of	WO 1990-US3451	19900618
		CIP of	US 1991-711334	19910606
		Div ex	US 1993-95734	19930722
			US 1995-444623	19950519
US 6022745	A	CIP of	US 1988-216390	19880707
		CIP of	US 1988-223089	19880722
		CIP of	US 1989-361944	19890605
		CIP of	US 1989-367894	19890619
		CIP of	US 1991-711334	19910606
		Cont of	US 1993-95734	19930722
		Cont of	WO 1994-US8267	19940722
			US 1995-471869	19950607
US 6355486	B1	CIP of	US 1987-20451	19870302
		CIP of	US 1988-163546	19880303
		CIP of	US 1988-216390	19880707
		CIP of	US 1988-223089	19880722
		CIP of	US 1989-361944	19890605
		CIP of	US 1989-367894	19890619
		CIP of	US 1991-711334	19910606

	Cont of	US 1993-95734	19930722
	Cont of	US 1995-471869	19950607
		US 1999-342563	19990629

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 710287	A1 Based on	WO 9503417
US 5866403	A CIP of	US 4816708
	CIP of	US 5504005
US 6022745	A CIP of	US 5504005
	Cont of	US 5807723
US 6355486	B1 CIP of	US 5504005
	Cont of	US 5807723
	Cont of	US 6022745

PRIORITY APPLN. INFO: US 1993-95734 19930722; US
1987-20451 19870302; US
1988-163546 19880303; US
1988-216390 19880614; US
1988-223089 19880722; US
1989-361944 19890605; US
1989-367894 19890619; WO
1990-US3451 19900618; US
1991-711334 19910606; US
1995-444623 19950519; US
1995-471869 19950607; US
1999-342563 19990629

AN 1995-075243 [10] WPIDS
CR 1988-271166 [38]; 1990-051704 [07]; 1991-022237 [03]; 1995-075244 [10]
AB WO 9503417 A UPAB: 20020403

Transforming a slow-growing mycobacterium (I) with heterologous DNA (II), comprises: (a) combining (I) and (II) to be **transformed** into (I), thereby producing a combination; and (b) subjecting the combination produced to electroporation in water, under conditions sufficient for introduction of (II) into (I). Also claimed are: (A) a method of producing attenuated mycobacterium tuberculosis (Mt) comprising inactivating or deleting in Mt DNA selected from the gp. consisting of: the Kat G gene; the Hsp60 gene, aro A, lys A, ura A and DNA associated with entry into and survival inside cells; (B) a DNA **construct** consisting of (a) DNA homologous to genomic DNA of a slow-growing mycobacterium, which is a genetic marker, and (b) DNA **non-homologous** to genomic DNA of the slow-growing mycobacterium, where the DNA **non-homologous** to genomic DNA of (I) is flanked by the DNA homologous to genomic DNA of (I); (C) a homologously recombinant slow-growing mycobacterium having incorporated in it, heterologous DNA homologous to genomic DNA of the slow-growing mycobacterium; (D) isolated DNA of mycobacterial origin encoding orotidine-5'-monophosphate decarboxylase; and (E) isolated orotidine-5'-monophosphate decarboxylase of mycobacterial origin.

USE - (I) are useful as e.g. vehicles in which proteins encoded by the heterologous **non-homologous** DNA are expressed.
They are useful as vaccines, which express a polypeptide or protein of interest, such as an antigen of at least 1 pathogens (e.g. viruses, bacteria or mycobacteria) against which protection is desired. (I) can also be used to express enzymes, immunopotentiators, lymphokines, pharmacologic agents, antitumour agents or stress proteins. (I) can express polypeptides or proteins which are growth inhibitors or are cytocidal for tumour cells (e.g. A, B or C interferon, TNF or ILs) and, thus, are useful for treating certain human cancers (e.g. bladder cancers, melanomas).

ADVANTAGE - Vaccines produced are more efficient than presently used vaccines i.e. mycobacteria having adjuvant properties, they stimulate a recipient's immune system to respond to other antigens with great effectiveness. In addition, the mycobacterium stimulate long-term memory or immunity. This means that a single innoculation can be used to produce long-term sensitisation to protein antigen. This is useful against e.g. tetanus, and diphtheria toxins, pertussis, malaria, influenza, herpes virus and snake venoms.
Dwg.0/5

L24 ANSWER 15 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1993:249297 CAPLUS
DOCUMENT NUMBER: 118:249297
TITLE: Genetic **construct** for selection of homologous recombinants on a single selective medium
INVENTOR(S): Guerra, Daniel J.; Xiang, Chengbin
PATENT ASSIGNEE(S): Idaho Research Foundation, Inc., USA
SOURCE: PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9307266	A1	19930415	WO 1992-US8513	19921006
W: AT, AU, BB, BG, BR, CA, CH, CS, DE, DK, ES, FI, GB, HU, JP, KP, KR, LK, LU, MG, MN, MW, NL, NO, PL, RO, RU, SD, SE, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, SN, TD, TG				
AU 9227789	A1	19930503	AU 1992-27789	19921006
US 5527674	A	19960618	US 1994-236957	19940502
PRIORITY APPLN. INFO.:			US 1991-773333 A2	19911007
			WO 1992-US8513 A	19921006

AB The title genetic **construct** comprises a 1st gene for a pos. selectable genetic trait, and, optionally a 2nd desired gene, flanked by sequences homologous to sequences flanking an integration site in a target cell; and an antisense gene which produces a product antagonistic to the 1st gene. Those target cells which have incorporated the selectable gene by homologous recombination will survive the selection process. Those target cells which have incorporated the selectable gene by **non-homologous** recombination will have also incorporated the antisense **construct**. These cells, as well as nontransformants, will be killed during the selection process. This system is especially suitable for plant cell **transformation** because it obviates the necessity for screening all recombinants by Southern blotting, and because it provides a universal neg. selectable marker system. The principle on which this system is based was demonstrated in tobacco using a neomycin phosphotransferase gene fused to nopaline synthase promoter and terminator sequences and an antisense neomycin phosphotransferase gene fused to the 35S promoter.

L24 ANSWER 16 OF 19 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 93295431 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8515775
TITLE: Stable **transformation** of Trypanosoma brucei.
AUTHOR: ten Asbroek A L; Mol C A; Kieft R; Borst P
CORPORATE SOURCE: Division of Molecular Biology, The Netherlands Cancer Institute, Amsterdam.
SOURCE: Molecular and biochemical parasitology, (1993 May) 59 (1) 133-42.

Journal code: 8006324. ISSN: 0166-6851.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199307
ENTRY DATE: Entered STN: 19930806
Last Updated on STN: 19970203
Entered Medline: 19930720

AB We have further analyzed parameters affecting stable **transformation** of Trypanosoma brucei. Linear DNA was much more efficient than circular DNA and in the vast majority of **transformants** analyzed the plasmid DNA had inserted into the chromosomes by homologous recombination. The presence of **non-homologous** (vector) DNA at one or both ends of linear constructs inhibited **transformation** efficiency. Less than 1 kb of homologous flanking sequence was sufficient for efficient targeting of a marker gene into the tubulin gene array. When **transformants** with a single neomycin phosphotransferase (neo(r)) gene replacing a beta-tubulin gene were selected for higher levels of G418 resistance, the neo(r) gene was amplified and spread through the tubulin gene cluster. The additional neo(r) gene copies were adjacent in the tubulin gene array and were added to the array rather than replacing beta-tubulin genes. These results are compatible with asymmetric post-replication recombination (unequal sister chromatid exchange) as the mechanism for neo(r) gene amplification. Starting with a circular **construct** containing the neo(r) gene between tubulin intergenic regions, we obtained a single **transformant** that maintained the neo(r) genes as an extrachromosomal plasmid. We show this plasmid to consist of a circular pentamer of the input **construct**. All other attempts to derive a shuttle vector that replicates extrachromosomally in T. brucei were unsuccessful. Our experiments extend previous observations suggesting that T. brucei has a strong preference for chromosomal insertion of exogenous DNA by homologous recombination.

L24 ANSWER 17 OF 19 MEDLINE on STN DUPLICATE 6
ACCESSION NUMBER: 94033281 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8219042
TITLE: Down-regulation of two **non-homologous** endogenous tomato genes with a single chimaeric sense gene **construct**.
AUTHOR: Seymour G B; Fray R G; Hill P; Tucker G A
CORPORATE SOURCE: Department of Applied Biochemistry, University of Nottingham, School of Agriculture, Loughborough, Leics, UK.
SOURCE: Plant molecular biology, (1993 Oct) 23 (1) 1-9.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19940117
Entered Medline: 19931126

AB Tomatoes (Lycopersicon esculentum Mill cv. Ailsa Craig) were **transformed** with a gene **construct** having 244 bp of the 5' end of a polygalacturonase (PG) cDNA, coding for a 71 amino acid N-terminal extension to the mature protein, fused to 1320 bp of a pectin-esterase (PE) cDNA encoding the full sequence of the mature PE protein. This chimaeric gene was inserted in a sense orientation between a CaMV 35S promoter and terminator for constitutive expression. In **transformed** tomato plants expression of the endogenous PG and PE

genes in the fruit was inhibited; there was little or no observable PG and PE mRNA and a substantial reduction in the level of PG and PE enzyme activity. The transgene was expressed in the leaves of the **transformed** plants as demonstrated by the accumulation of mRNA, but no protein product could be identified. However, no transgene mRNA or protein were observed in the transgenic fruit. The paper represents the first report of the down-regulation of two **non-homologous** endogenous genes using a single gene **construct**. A sense gene **construct** was responsible for these effects. These findings are discussed in relation to possible mechanisms of action of co-suppression.

L24 ANSWER 18 OF 19 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 1992-415786 [50] WPIDS
DOC. NO. CPI: C1992-184571
TITLE: Genomic modification using DNA targetting for treating genetic disorder etc. - by using vector containing DNA with homology but different to a target locus and a marker gene.
DERWENT CLASS: B04 D16
INVENTOR(S): SMITHIES, O
PATENT ASSIGNEE(S): (CELL-N) CELL GENESYS INC
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9220808	A1	19921126	(199250)*	EN	42
RW: AT BE CH DE DK ES FR GB GR IT LU MC NL SE					
W: AU CA JP KR NO					
AU 9221402	A	19921230	(199313)		
EP 539573	A1	19930505	(199318)	EN	42
R: AT BE CH DE DK ES FR GB GR IT LI LU MC NL SE					
EP 539573	A4	19931229	(199528)		
AU 664847	B	19951207	(199605)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9220808	A1	WO 1992-US4054	19920513
AU 9221402	A	AU 1992-21402	19920513
		WO 1992-US4054	19920513
EP 539573	A1	EP 1992-913238	19920513
		WO 1992-US4054	19920513
EP 539573	A4	EP 1992-913238	
AU 664847	B	AU 1992-21402	19920513

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9221402	A	Based on	WO 9220808
EP 539573	A1	Based on	WO 9220808
AU 664847	B	Previous Publ.	AU 9221402
		Based on	WO 9220808

PRIORITY APPLN. INFO: US 1991-700501 19910515
AN 1992-415786 [50] WPIDS
AB WO 9220808 A UPAB: 19931116
A method for introducing changes at a target locus (TL) in a chromosome of a viable mammalian cell is new, and comprises: (i) **transforming**

the cell with a linear DNA **construct** containing a sequence with at least 50 bp of homology with an indigenous region (IR) of the TL, but different from the TL, and a marker gene. The **construct** is an omega- or O-targeting vector, where a **non-homologous** sequence forms an internal or external loop, respectively; (ii) growing the cells for selection of marker-containing cells; and (iii) isolating cells containing the change in the IR by identifying the presence of the **construct** sequence at the locus. When the **construct** is an omega-vector, the **non-homologous** region is at a site which does not interfere with the functioning of the TL.

Also new is a linear targeting vector **construct** comprising: a wild-type structural gene sequence (I) of a gene associated with a genetic disease resulting from a sequence difference, (I) is homologous at the chromosomal locus (CL) of the difference; at least one marker gene for positive selection; and flanking homologous sequences (HS), those proximal to the terminals of the vector **construct** are either distal at the CL to define an omega-targeting vector or proximal for an O-targeting vector.

USE/ADVANTAGE - Enables modifications of genomic target sites, for correcting and treating genetic disorders, mapping chromosomes, identifying loci, etc.. The vectors either allow for retention of the marker gene without interference to the locus, or for excision of the marker(s)

Dwg.0/0

ABEQ EP 539573 A UPAB: 19931112

A method for introducing changes at a target locus (TL) in a chromosome of a viable mammalian cell comprises: (i) **transforming** the cell with a linear DNA **construct** containing, a sequence with at least 50 bp of homology with an indigenous region (IR) of the TL, but different from the TL, and a marker gene. The **construct** is an omega- or O-targeting vector, where a **non-homologous** sequence forms an internal or external loop, respectively; (ii) growing the cells for selection of marker-contg. cells; and (iii) isolating cells contg. the change in the IR by identifying the presence of the **construct** sequence at the locus. When the **construct** is an omega-vector, the **non-homologous** region is at a site which does not interfere with the functioning of the TL.

Also new is a linear targeting vector **construct** comprising: a wild-type structural gene sequence (I) of a gene associated with a genetic disease resulting from a sequence difference. (I) is homologous at the chromosomal locus (CL) of the difference; at least one marker gene for positive selection; and flanking homologous sequences (HS), those proximal to the terminals of the vector **construct** are either distal at the CL to define an omega-targeting vector or proximal for an O-targeting vector.

USE/ADVANTAGE - Enables modifications of genomic target sites, for correcting and treating genetic disorders, mapping chromosomes, identifying loci, etc. The vectors either allow for retention of the marker gene without interference to the locus, or for excision of the marker(s).

Dwg.0/0

L24 ANSWER 19 OF 19 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1991:529098 CAPLUS
DOCUMENT NUMBER: 115:129098
TITLE: Targeted disruption of a human interferon-inducible gene detected by secretion of human growth hormone
AUTHOR(S): Itzhaki, Jane E.; Porter, Andrew C. G.
CORPORATE SOURCE: Dep. Biochem., Univ. Oxford, Oxford, OX1 3QU, UK
SOURCE: Nucleic Acids Research (1991), 19(14), 3835-42
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal

LANGUAGE: English

AB A new method is described for the sib-selection of targeted mammalian cells that have undergone homologous recombination (HR) with a transfected DNA **construct**. This method has been used to disrupt the 6-16 gene, an interferon (IFN)-inducible gene of unknown function, in two different human cell lines. Disruption was caused by integration of a targeting **construct** containing a promoterless gene for human growth hormone (hGH) which was expressed after HR with the 6-16 gene. Homologous recombinants were detected in pools of **non-homologous** recombinants by the appearance of hGH in the growth medium after the addition of IFN. Secondary and tertiary rounds of hGH assays were used to sib-select 9 homologous recombinants that were shown to have 1, 2 or 3 copies of the targeting **construct** integrated at the 6-16 locus. The method, which should be applicable to other transcribed targets, provides an alternative to selection methods, and offers advantages over other screening methods in being simple, rapid, sensitive and reliable.

=> d his

(FILE 'HOME' ENTERED AT 11:08:09 ON 11 MAR 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:08:23 ON 11 MAR 2005

L1 0 INITIAT? (W) DNA (W) UPTAKE
L2 373 INITIAT? (S) DNA (S) UPTAKE
L3 4746 NON (W) HOMOLOGOUS
L4 0 L2 AND L3
L5 209 STUFFER AND DNA
L6 0 L5 AND L2
L7 2254 DNA (W) UPTAKE
L8 1 L7 AND L3
L9 0 L5 AND L7
L10 18629 DNA (S) UPTAKE
L11 0 L10 AND L5
L12 7 L10 AND L3
L13 4 DUP REM L12 (3 DUPLICATES REMOVED)
E DIAZ (W) TORRES MARIA/AU
E DIAZ TORRES MARIA/AU
L14 54 E1-E4
L15 23 DUP REM L14 (31 DUPLICATES REMOVED)
L16 2 TRANSFORM? AND L15
L17 0 L3 AND L5
L18 1447160 TRANSFORM?
L19 470 L3 AND L18
L20 0 L19 AND L5
L21 5 L19 AND L10
L22 2 DUP REM L21 (3 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:39:56 ON 11 MAR 2005

L23 33 CONSTRUCT AND L19
L24 19 DUP REM L23 (14 DUPLICATES REMOVED)

=> flank? and l19
L25 63 FLANK? AND L19

=> dub rem l25
MISSING OPERATOR REM L25
The search profile that was entered contains terms or

nested terms that are not separated by a logical operator.

=> dup rem l25
PROCESSING COMPLETED FOR L25
L26 27 DUP REM L25 (36 DUPLICATES REMOVED)

=> t ti l26 1-27

L26 ANSWER 1 OF 27 MEDLINE on STN DUPLICATE 1
TI A rapid method for promoter exchange in Aspergillus nidulans using recombinant PCR.

L26 ANSWER 2 OF 27 CAPLUS COPYRIGHT 2005 ACS on STN
TI Protein and cDNA sequences of a novel human protooncogene HPP1, and use in cancer diagnosis and therapy

L26 ANSWER 3 OF 27 MEDLINE on STN DUPLICATE 2
TI Directional ligation of long-**flanking** homology regions to selection cassettes for efficient targeted gene-disruption in Candida albicans.

L26 ANSWER 4 OF 27 MEDLINE on STN DUPLICATE 3
TI Efficient gene targeting in Kluyveromyces lactis.

L26 ANSWER 5 OF 27 MEDLINE on STN DUPLICATE 4
TI Cloning of glyceraldehyde-3-phosphate dehydrogenase gene and use of the gpd promoter for **transformation** in Flammulina velutipes.

L26 ANSWER 6 OF 27 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Generating genetically modified vertebrate precursor lymphocytes for producing any heterologous antibody or binding protein comprises effecting differentiation of the precursor lymphocytes into mature lymphoid lineage cells.

L26 ANSWER 7 OF 27 CAPLUS COPYRIGHT 2005 ACS on STN
TI Bacillus **transformation** and construction of mutant libraries

L26 ANSWER 8 OF 27 MEDLINE on STN
TI DNA substrate dependence of p53-mediated regulation of double-strand break repair.

L26 ANSWER 9 OF 27 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Insertional mutagenesis in the n-alkane-assimilating yeast Yarrowia lipolytica: Generation of tagged mutations in genes involved in hydrophobic substrate utilization.

L26 ANSWER 10 OF 27 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI **Non-homologous transformation** of Yarrowia comprises **transforming** a Yarrowia strain lacking zeta sequences with a recombinant vector harboring a gene insert **flanked** by zeta sequences.

L26 ANSWER 11 OF 27 MEDLINE on STN DUPLICATE 5
TI PCR-mediated direct gene disruption in Schizosaccharomyces pombe.

L26 ANSWER 12 OF 27 MEDLINE on STN DUPLICATE 6
TI Heterologous HIS3 marker and GFP reporter modules for PCR-targeting in Saccharomyces cerevisiae.

L26 ANSWER 13 OF 27 CAPLUS COPYRIGHT 2005 ACS on STN
TI Characterization of promoters and stable transfection by homologous and nonhomologous recombination in Plasmodium falciparum

L26 ANSWER 14 OF 27 MEDLINE on STN DUPLICATE 7
TI In vivo intermolecular recombination in Escherichia coli: application to plasmid constructions.

L26 ANSWER 15 OF 27 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Slow-growing mycobacteria **transformed** with heterologous DNA - useful as vaccines in which the mycobacteria stimulate long-term memory or immunity.

L26 ANSWER 16 OF 27 MEDLINE on STN DUPLICATE 8
TI Stable DNA **transformation** of Toxoplasma gondii using phleomycin selection.

L26 ANSWER 17 OF 27 MEDLINE on STN DUPLICATE 9
TI Cointegration of **transforming** DNAs in Aspergillus nidulans: a model using autonomously-replicating plasmids.

L26 ANSWER 18 OF 27 CAPLUS COPYRIGHT 2005 ACS on STN
TI Genetic construct for selection of homologous recombinants on a single selective medium

L26 ANSWER 19 OF 27 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Purposive genetic modification of Ashbya (A) gossypii - by vectors containing insertable DNA within A. gossypii gene region, pref. from transcription elongation factor, useful in riboflavin production.

L26 ANSWER 20 OF 27 CAPLUS COPYRIGHT 2005 ACS on STN
TI Characterization of two identical independent **non-homologous** integration sites in mouse embryonic stem cells

L26 ANSWER 21 OF 27 MEDLINE on STN DUPLICATE 10
TI Stable **transformation** of Trypanosoma brucei.

L26 ANSWER 22 OF 27 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Genomic modification using DNA targetting for treating genetic disorder etc. - by using vector containing DNA with homology but different to target locus and a marker gene.

L26 ANSWER 23 OF 27 MEDLINE on STN DUPLICATE 11
TI The non-conserved region of cucumopine-type Agrobacterium rhizogenes T-DNA is responsible for hairy root induction.

L26 ANSWER 24 OF 27 MEDLINE on STN DUPLICATE 12
TI Molecular **transformation** of Fusarium solani with an antibiotic resistance marker having no fungal DNA homology.

L26 ANSWER 25 OF 27 MEDLINE on STN DUPLICATE 13
TI Effect of DNA damage on stable **transformation** of mammalian cells with integrative and episomal plasmids.

L26 ANSWER 26 OF 27 MEDLINE on STN DUPLICATE 14
TI Excision of integrated simian virus 40 DNA involving homologous recombination between viral DNA sequences.

L26 ANSWER 27 OF 27 MEDLINE on STN
TI Nucleotide sequences at host-proviral junctions for mouse mammary tumour virus.

=> l24 and l26
L27 6 L24 AND L26

=> t ti l27 1-6

L27 ANSWER 1 OF 6 MEDLINE on STN
TI Efficient gene targeting in Kluyveromyces lactis.

L27 ANSWER 2 OF 6 MEDLINE on STN
TI Stable **transformation** of Trypanosoma brucei.

L27 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
TI Genetic **construct** for selection of homologous recombinants on a single selective medium

L27 ANSWER 4 OF 6 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Generating genetically modified vertebrate precursor lymphocytes for producing any heterologous antibody or binding protein comprises effecting differentiation of the precursor lymphocytes into mature lymphoid lineage cells.

L27 ANSWER 5 OF 6 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Slow-growing mycobacteria **transformed** with heterologous DNA - useful as vaccines in which the mycobacteria stimulate long-term memory or immunity.

L27 ANSWER 6 OF 6 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Genomic modification using DNA targetting for treating genetic disorder etc. - by using vector containing DNA with homology but different to a target locus and a marker gene.

=> l26 not l27
L28 21 L26 NOT L27

=> d ibib abs l28 1-21

L28 ANSWER 1 OF 21 MEDLINE on STN
ACCESSION NUMBER: 20046170S4 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15588991
TITLE: A rapid method for promoter exchange in Aspergillus nidulans using recombinant PCR.
AUTHOR: Zarrin Majid; Leeder Abigail C; Turner Geoffrey
CORPORATE SOURCE: Department of Molecular Biology and Biotechnology, Firth Court, University of Sheffield S10 2TN, UK.
SOURCE: Fungal genetics and biology : FG & B, (2005 Jan) 42 (1) 1-8.
Journal code: 9607601. ISSN: 1087-1845.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: NONMEDLINE; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20041220
Last Updated on STN: 20050202
AB Recombinant PCR has been used to generate linear fragments for promoter replacement by **transformation** in Aspergillus nidulans. A cassette vector carrying the pyr-4 **non-homologous** selectable marker and conditional promoter Pr-alcA was constructed for use as a template for PCR, and is suitable for testing the function of essential genes. Two genes involved in polar growth, cotA and bemA, were used to assess the system. Efficient targeting was possible with both genes using approximately 500bp of **flanking** homologous sequence. Depending on yield, the linear PCR product could be used directly for **transformation**, or after first cloning into a suitable vector.

bemA, a putative homologue of the Saccharomyces cerevisiae BEM1 gene was identified through sequence comparison. In A. nidulans, this protein appears to have a similar role to the yeast Bem1p, which acts as a scaffold protein involved in the establishment of cell polarity.

L28 ANSWER 2 OF 21 MEDLINE on STN
ACCESSION NUMBER: 2004482938 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15450191
TITLE: Directional ligation of long-**flanking** homology regions to selection cassettes for efficient targeted gene-disruption in Candida albicans.
AUTHOR: Taneja Vibha; Paul Sanjoy; Ganesan K
CORPORATE SOURCE: Institute of Microbial Technology, Sector 39-A, Chandigarh 160 036, India.
SOURCE: FEMS yeast research, (2004 Sep) 4 (8) 841-7.
Journal code: 101085384. ISSN: 1567-1356.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200412
ENTRY DATE: Entered STN: 20040929
Last Updated on STN: 20041221
Entered Medline: 20041220

AB PCR-product directed gene disruption with a marker cassette having short homology regions is often used in Candida albicans. However, it is quite inefficient due to the high frequency of **non-homologous** recombination at non-targeted loci, which necessitates extensive screening to identify the correct disruptants. Thus, many PCR-based methods to introduce long **flanking** homology regions have been developed to increase the frequency of integration at the targeted loci. However, these methods are not that amenable for use with the widely employed C. albicans marker cassettes having direct repeats, as these repeats tend to recombine during PCR, resulting in shorter amplified products without the selection marker. To circumvent this limitation, we have developed a dinucleotide-sticky-end-ligation strategy to add one **flanking** homology region to one side of the selection cassette, and the other **flanking** homology region to the other side of the selection cassette. This method involves release of the selection cassette from the plasmid by digestion with two different restriction enzymes, followed by partial fill-in, to provide a unique two base overhang at each end of the cassette. The **flanking** homology regions, corresponding to the gene to be disrupted, are individually PCR-amplified, and treated with T4-DNA Polymerase in the presence of appropriate dNTPs to yield two base-5' overhangs. The primers used for the PCR have additional bases at the 5' ends such that after T4 DNA Polymerase treatment, the two **flanks** will have distinct overhangs compatible with the overhangs of the partially filled-in selection cassette. The selection cassette and the **flanks** are then ligated together and directly used to **transform** C. albicans. We have successfully used this method for disruption of several C. albicans genes. We have also used this method to recreate insertion mutations obtained with transposons to reconfirm the mutant phenotypes. This approach can be extended to other organisms like Schizosaccharomyces pombe which also require long **flanking** regions of homology for targeted gene disruption.

L28 ANSWER 3 OF 21 MEDLINE on STN
ACCESSION NUMBER: 2004466796 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15168094
TITLE: Cloning of glyceraldehyde-3-phosphate dehydrogenase gene and use of the gpd promoter for **transformation** in Flammulina velutipes.

AUTHOR: Kuo Chun-Yi; Chou Shu-Yu; Huang Ching-Tsan
CORPORATE SOURCE: Institute of Microbiology and Biochemistry, National Taiwan University, No 1, Section 4, Roosevelt Road, 106, Taipei.
SOURCE: Applied microbiology and biotechnology, (2004 Oct) 65 (5) 593-9. Electronic Publication: 2004-05-27.
Journal code: 8406612. ISSN: 0175-7598.
PUB. COUNTRY: Germany: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: NONMEDLINE; IN-PROCESS; NONINDEXED; Priority Journals
OTHER SOURCE: GENBANK-AF515622
ENTRY DATE: Entered STN: 20040921
Last Updated on STN: 20041219

AB The glyceraldehyde-3-phosphate dehydrogenase gene of Flammulina velutipes was isolated. The complete gpd sequence (from ATG to TAA) was 1,489 bp in length and contained nine introns. The locations of these nine introns were similar to those of other basidiomycetes, which might reflect the evolutionary divergence of these mushrooms. The F. velutipes gpd gene was found to encode a protein of 339 amino acids and its putative amino acid sequence revealed a high similarity to an analogous protein deriving from other basidiomycetes. Results of Southern blot analysis suggested that there existed only one copy of the gpd gene in the genome of F. velutipes and that there was one typical TATA box and two CAAT boxes located in the 5' **flanking** region. The F. velutipes gpd promoter was fused to a hygromycin B phosphotransferase gene (hph) derived from Escherichia coli as a selection marker. Using the resulting construction, hph was efficiently **transformed** into F. velutipes by basidiospore electroporation. No false-positive antibiotic-resistant cultures were detected by PCR amplification and the hygromycin resistance trait was maintained stably during mitotic cell division for 3 months. Southern analysis of **transformants** indicated the integration of gene might occur by **non-homologous** recombination. This rapid and convenient electroporation procedure offers new prospects for the genetic manipulation and a tool for tagging genes of this important edible mushroom species. Sequence data will appear in the DDBJ/EMBL/GenBank nucleotide sequence database under accession number AF515622.

L28 ANSWER 4 OF 21 MEDLINE on STN
ACCESSION NUMBER: 2002413475 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12167722
TITLE: DNA substrate dependence of p53-mediated regulation of double-strand break repair.
AUTHOR: Akyuz Nuray; Boehden Gisa S; Susse Silke; Rimek Andreas; Preuss Ute; Scheidtmann Karl-Heinz; Wiesmuller Lisa
CORPORATE SOURCE: Universitatsfrauenklinik, D-89075 Ulm, Germany.
SOURCE: Molecular and cellular biology, (2002 Sep) 22 (17) 6306-17.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200209
ENTRY DATE: Entered STN: 20020809
Last Updated on STN: 20020910
Entered Medline: 20020909

AB DNA double-strand breaks (DSBs) arise spontaneously after the conversion of DNA adducts or single-strand breaks by DNA repair or replication and can be introduced experimentally by expression of specific endonucleases. Correct repair of DSBs is central to the maintenance of genomic integrity in mammalian cells, since errors give rise to translocations, deletions, duplications, and expansions, which accelerate the multistep process of

tumor progression. For p53 direct regulatory roles in homologous recombination (HR) and in **non-homologous** end joining (NHEJ) were postulated. To systematically analyze the involvement of p53 in DSB repair, we generated a fluorescence-based assay system with a series of episomal and chromosomally integrated substrates for I-SceI meganuclease-triggered repair. Our data indicate that human wild-type p53, produced either stably or transiently in a p53-negative background, inhibits HR between substrates for conservative HR (cHR) and for gene deletions. NHEJ via microhomologies **flanking** the I-SceI cleavage site was also downregulated after p53 expression. Interestingly, the p53-dependent downregulation of homology-directed repair was maximal during cHR between sequences with short homologies. Inhibition was minimal during recombination between substrates that support reporter gene reconstitution by HR and NHEJ. p53 with a hotspot mutation at codon 281, 273, 248, 175, or 143 was severely defective in regulating DSB repair (frequencies elevated up to 26-fold). For the transcriptional transactivation-inactive variant p53(138V) a defect became apparent with short homologies only. These results suggest that p53 plays a role in restraining DNA exchange between imperfectly homologous sequences and thereby in suppressing tumorigenic genome rearrangements.

L28 ANSWER 5 OF 21 MEDLINE on STN
ACCESSION NUMBER: 97435480 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9290211
TITLE: Heterologous HIS3 marker and GFP reporter modules for PCR-targeting in Saccharomyces cerevisiae.
AUTHOR: Wach A; Brachat A; Alberti-Segui C; Rebischung C; Philippsen P
CORPORATE SOURCE: Institut fur Angewandte Mikrobiologie, Universitat Basel, Switzerland.
SOURCE: Yeast (Chichester, England), (1997 Sep 15) 13 (11) 1065-75. Journal code: 8607637. ISSN: 0749-503X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ002681; GENBANK-AJ002682; GENBANK-AJ002683
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980130
Last Updated on STN: 20000303
Entered Medline: 19980121

AB We have fused the open reading frames of his3-complementing genes from Saccharomyces kluyveri and Schizosac-charomyces pombe to the strong TEF gene promotor of the filamentous fungus Ashbya gossypii. Both chimeric modules and the cognate S. kluyveri HIS3 gene were tested in **transformations** of his3 S. cerevisiae strains using PCR fragments **flanked** by 40 bp target guide sequences. The 1.4 kb chimeric Sz. pombe module (HIS3MX6) performed best. With less than 5% incorrectly targeted **transformants**, it functions as reliably as the widely used geniticin resistance marker kanMX. The rare false-positive His+ **transformants** seem to be due to **non-homologous** recombination rather than to gene conversion of the mutated endogenous his3 allele. We also cloned the green fluorescent protein gene from Aequorea victoria into our pFA-plasmids with HIS3MX6 and kanMX markers. The 0.9 kb GFP reporters consist of wild-type GFP or GFP-S65T coding sequences, lacking the ATG, fused to the S. cerevisiae ADH1 terminator. PCR-synthesized 2.4 kb-long double modules **flanked** by 40-45 bp-long guide sequences were successfully targeted to the carboxy-terminus of a number of S. cerevisiae genes. We could estimate that only about 10% of the **transformants** carried inactivating mutations in the GFP reporter.

L28 ANSWER 6 OF 21 MEDLINE on STN
ACCESSION NUMBER: 97175817 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9023122
TITLE: PCR-mediated direct gene disruption in Schizosaccharomyces pombe.
AUTHOR: Kaur R; Ingavale S S; Bachhawat A K
CORPORATE SOURCE: Institute of Microbial Technology, Sector 39-A, Chandigarh 160 036, India.
SOURCE: Nucleic acids research, (1997 Mar 1) 25 (5) 1080-1.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970424
Last Updated on STN: 20030214
Entered Medline: 19970414

AB We have examined the feasibility and efficiency of PCR-mediated direct gene disruptions in the fission yeast Schizosaccharomyces pombe. In the present study, the S.pombe ura4+ gene was amplified by PCR with oligonucleotides that had short **flanking** regions (approximately 40 bp) to the target gene. Using this purified PCR product we were able to disrupt genes in an S. pombe strain bearing aura4 deletion, with an efficiency ranging between 1 and 3% among selected **transformants** . The results indicated that despite S.pombe's preference for **non -homologous** or illegitimate recombination, even very short stretches of homologous regions could be used to target genes at a defined frequency in this organism. The successful disruption of four independent genes (sts1+, gcs1+, gsh2+and hmt1+) by this method further demonstrates that, despite the relatively low efficiency, the method is very feasible, and it's simplicity, especially when coupled to phenotype-based screening, should greatly facilitate disruption of genes in S.pombe.

L28 ANSWER 7 OF 21 MEDLINE on STN
ACCESSION NUMBER: 96200853 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8621087
TITLE: In vivo intermolecular recombination in Escherichia coli: application to plasmid constructions.
AUTHOR: Degryse E
CORPORATE SOURCE: Yeast Department, Transgene SA, Strasbourg, France.
SOURCE: Gene, (1996 Apr 17) 170 (1) 45-50.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199606
ENTRY DATE: Entered STN: 19960627
Last Updated on STN: 19960627
Entered Medline: 19960620

AB Repair of a double-strand break (DSB) was investigated by intermolecular recombination in Escherichia coli (Ec) recBC sbcBC cells with restriction enzyme-cleaved model plasmids. Circular plasmids were generated when a linearized plasmid (vector) containing an origin of replication was co-**transformed** with a DNA fragment (template) containing a homologous sequence. The influence of the position of the DSB in the vector was analyzed using templates which contain various genetic markers, **non-homologous** sequences and/or deletions relative to the vector. In all cases, when a DSB occurs within a marker, this marker is lost in the resulting plasmid, whereas markers **flanked** by homologous regions located in the vicinity of a DSB are transmitted.

Insertions (deletions), substitutions and shuffling of genetic markers are possible by in vivo recombination using Ec and can be applied to plasmid constructions. It is shown that recombination can occur from both template ends or from one vector and one template end. A D-loop nuclease is suggested to participate in the resolution of the recombination intermediates.

L28 ANSWER 8 OF 21 MEDLINE on STN
ACCESSION NUMBER: 96096523 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8522178
TITLE: Stable DNA **transformation** of Toxoplasma gondii using phleomycin selection.
AUTHOR: Messina M; Niesman I; Mercier C; Sibley L D
CORPORATE SOURCE: Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, MO 63110, USA.
CONTRACT NUMBER: AI36629 (NIAID)
SOURCE: Gene, (1995 Nov 20) 165 (2) 213-7.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 19960219
Last Updated on STN: 19990129
Entered Medline: 19960122

AB Toxoplasma gondii (Tg) is an obligate intracellular protozoan parasite that is an important opportunistic pathogen in humans. To provide additional tools for molecular genetic analysis, we have developed a set of vectors for DNA **transformation** in Tg based on selection with the antibiotic phleomycin (Ph). These new vectors rely on the **flanking** sequences from the parasite genes GRA1, GRA2 or SAG1 to drive expression of the Tn5 ble gene encoding resistance to the DNA intercalating drug Ph (PhR). Treatment of extracellular parasites was used to select stable PhR **transformants** by plaque formation on host cell monolayers. Transfection of linear or circular forms of the pGRA1/ble, pGRA2/ble or pSAG1/ble vectors by electroporation resulted in stable **transformation** with an efficiency of approx. 10(-4)/micrograms DNA. Stable **transformants** contained 1-5 copies of ble that were integrated at **non-homologous** sites in the parasite nuclear genome. Ble provides a new dominant selectable marker for safe, efficient and rapid isolation of stable DNA **transformants** in Tg.

L28 ANSWER 9 OF 21 MEDLINE on STN
ACCESSION NUMBER: 95188273 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7882430
TITLE: Cointegration of **transforming** DNAs in Aspergillus nidulans: a model using autonomously-replicating plasmids.
AUTHOR: Aleksenko A Y
CORPORATE SOURCE: Institute of Genetics and Selection of Industrial Microorganisms, Moscow, Russia.
SOURCE: Current genetics, (1994 Oct) 26 (4) 352-8.
Journal code: 8004904. ISSN: 0172-8083.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199504
ENTRY DATE: Entered STN: 19950425
Last Updated on STN: 19950425
Entered Medline: 19950411

AB **Transforming** DNAs form cointegrates in Aspergillus nidulans by homologous and **non-homologous** recombination as well as by end-to-end ligation of linear fragments. This process has been studied by means of a model in which the linkage of a marker gene to the origin of autonomous replication AMA1 was selected for. Recombinant plasmids were rescued into Escherichia coli and subjected to restriction mapping and sequence analysis. It was shown that circular DNA molecules recombined predominantly within homologous fragments. Linear DNA fragments integrated into circular plasmids by invasion of their ends into random **non-homologous** sites, but exhibited some bias in choice of a target sequence. Cointegrates of multiple plasmid copies were often observed. In some of the plasmids analysed, short duplications of the target sequence **flanking** an inserted linear DNA fragment have been revealed.

L28 ANSWER 10 OF 21 MEDLINE on STN
ACCESSION NUMBER: 91346711 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2102883
TITLE: The non-conserved region of cucumopine-type Agrobacterium rhizogenes T-DNA is responsible for hairy root induction.
AUTHOR: Failla M C; Maimone F; De Paolis A; Costantino P; Cardarelli M
CORPORATE SOURCE: Dip. Genetica e Biologia Molecolare, Universita La Sapienza, Roma, Italy.
SOURCE: Plant molecular biology, (1990 Nov) 15 (5) 747-53. Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199110
ENTRY DATE: Entered STN: 19911020
Last Updated on STN: 19911020
Entered Medline: 19911001

AB The T-DNA regions of three strains of Ri plasmids 1855, 8196, 2659 (agropine, mannopine and cucumopine type respectively) share two highly conserved regions **flanking** a **non-homologous** central part. We have cloned segments of the cucumopine Ri plasmid 2659 T-DNA in the binary vector system Bin 19 and infected carrot discs with recombinant Agrobacterium strains. We show here that the central non-conserved region is crucial in hairy root induction as it is sufficient to induce rooting on the apical (auxin-rich) surface of carrot discs; in order to observe rooting on the basal (auxin-depleted) side of the discs, a longer T-DNA fragment, also encompassing part of the right conserved region, had to be utilized in conjunction with a Agrobacterium strain carrying aux genes. Differences of growth properties in culture are exhibited by roots **transformed** with different fragments of pRi 2659 T-DNA, although all **transformed** roots show the plagiotropic behaviour typical of hairy roots.

L28 ANSWER 11 OF 21 MEDLINE on STN
ACCESSION NUMBER: 89376617 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2550150
TITLE: Molecular **transformation** of Fusarium solani with an antibiotic resistance marker having no fungal DNA homology.
AUTHOR: Marek E T; Schardl C L; Smith D A
CORPORATE SOURCE: Department of Plant Pathology, University of Kentucky, Lexington 40546-0091.
SOURCE: Current genetics, (1989 Jun) 15 (6) 421-8. Journal code: 8004904. ISSN: 0172-8083.
PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198910
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19990129
Entered Medline: 19891026

AB A vector was constructed for **transformation** of the plant pathogenic fungus Fusarium solani. The promoter 35Sp, from cauliflower mosaic virus, was fused to the bacterial gene APH(3')II, which confers resistance to the aminoglycoside antibiotic G418. Two **transformation** procedures were developed: one using isolated fungal protoplasts, the other using germinated fungal spores. A **transformation** frequency of 3.3 G418-resistant colonies were obtained per microgram DNA. Of 14 colonies analyzed, 12 had vector sequences integrated into their high molecular weight DNA, and 2 were untransformed. Integration was sometimes accompanied by rearrangements of both the vector and **flanking** fungal DNAs. Primer-extension analysis of the mRNA from one **transformant** revealed two putative transcription initiation sites in the chimeric APH(3')II gene. Both sites differed from the normal initiation site in plants. This vector will be useful in **transformation** systems in which integration by **non-homologous** recombination is desired.

L28 ANSWER 12 OF 21 MEDLINE on STN
ACCESSION NUMBER: 89199653 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2539484
TITLE: Excision of integrated simian virus 40 DNA involving homologous recombination between viral DNA sequences.
AUTHOR: Dora S; Schwarz C; Knippers R
CORPORATE SOURCE: Fakultat fur Biologie, Universitat Konstanz, F.R.G.
SOURCE: Journal of molecular biology, (1989 Mar 5) 206 (1) 81-90.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198905
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19990129
Entered Medline: 19890525

AB We have investigated the structure of simian virus 40 (SV40) DNA integrated into the genome of **transformed** mouse mKS-A cells. We have identified at least six independent integration units containing intact or truncated SV40 DNA sequences. One integration unit was isolated from a genomic mKS-A cell library and investigated by restriction enzyme analysis and partial nucleotide sequencing. This integration unit contains one apparently intact SV40 genome **flanked** on both sides by truncated versions of the SV40 genome. One of the **flanking** elements contains a large deletion in the SV40 "late" region and an abbreviated SV40 "early" region. This element was efficiently excised and mobilized after fusion of mKS-A to COS cells. The excision products invariably included the entire SV40 early region even though they were derived from an integrated element lacking this part of the SV40 genome. An analysis of this discrepancy led to the conclusion that the early region sequences were acquired by homologous recombination and, furthermore, that homologous excisional recombination was clearly preferred over **non-homologous** recombination.

L28 ANSWER 13 OF 21 MEDLINE on STN
ACCESSION NUMBER: 89181762 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2927424

TITLE: Effect of DNA damage on stable **transformation** of mammalian cells with integrative and episomal plasmids.
AUTHOR: Vos J M; Hanawalt P C
CORPORATE SOURCE: Department of Biological Sciences, Stanford University, CA 94305-5020.
CONTRACT NUMBER: CA35744-03 (NCI)
SOURCE: Mutation research, (1989 Mar-May) 220 (2-3) 205-20.
Journal code: 0400763. ISSN: 0027-5107.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198905
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890510

AB The efficiency of stable **transformation** of human cells by integrative (non-replicating) plasmids carrying a selectable gene has been shown to be markedly enhanced by the introduction into the plasmid DNA of bulky damage, such as cyclobutane pyrimidine dimers or psoralen photoadducts. Enhanced **transformation** (ET) occurs in all human cells tested, including DNA repair-deficient cells from the hereditary syndrome xeroderma pigmentosum, but significantly less, if at all, in rodent cells. ET has been observed with a variety of integrative plasmid constructs, suggesting the generality of the phenomenon; as expected, ET is due to an increase in the number of cells carrying integrated plasmid sequences. In contrast to integrative plasmids, stable **transformation** by episomal (autonomously replicating) plasmids derived from the Epstein-Barr virus is only depressed by the introduction of photoproducts; furthermore, pronounced inactivation of **transformation** mediated by episomal plasmids becomes apparent in xeroderma pigmentosum cells. Altogether, these results suggest that DNA damage increases the probability of stable insertion of heterologous non-replicating DNA into human chromosomes. Moreover, the differential sensitivity to DNA damage of human cell **transformation** mediated by integrative versus episomal plasmids suggests caution in using such assay to measure host cell reactivation capacity; processing of DNA damage in mammalian cells might differ significantly between intra- versus extra-chromosomal DNA. Since ET may be induced by damage outside the selectable gene carried on integrative plasmids, we propose a model that involves local disruption of chromatin structure by helix-distorting DNA lesions **flanking** actively transcribed sequences; alternatively, reorganization of such altered DNA structure might be favored by the presence of topoisomerase-like activities in the proximity of active genes. Because ET can also be induced by DNA damage to the recipient cells, it is speculated that similar mechanism(s) might be involved in the generation of other types of **non-homologous** DNA recombination in damaged human chromosomes, including oncogenic cell **transformation** mediated by integrative DNA viruses.

L28 ANSWER 14 OF 21 MEDLINE on STN
ACCESSION NUMBER: 81099020 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6256658
TITLE: Nucleotide sequences at host-proviral junctions for mouse mammary tumour virus.
AUTHOR: Majors J E; Varmus H E
CONTRACT NUMBER: 1T32 CA 09043 (NCI)
CA 12705 (NCI)
CA 19289 (NCI)
SOURCE: Nature, (1981 Jan 22) 289 (5795) 253-8.
Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198103
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19970203
Entered Medline: 19810324

AB Proviruses cloned from rat cells infected with mouse mammary tumour virus, a B-type retrovirus regulated by glucocorticoid hormones, show the structural features of transposable elements: short inverted repeats conclude long direct repeats at the ends of viral DNA, and short sequences of cellular DNA are duplicated during integration and **flank** each provirus. The integrative mechanism joins a precise site in viral DNA to **non-homologous** sites in host DNA.

L28 ANSWER 15 OF 21 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2001:420862 BIOSIS
DOCUMENT NUMBER: PREV200100420862
TITLE: Insertional mutagenesis in the n-alkane-assimilating yeast Yarrowia lipolytica: Generation of tagged mutations in genes involved in hydrophobic substrate utilization.
AUTHOR(S): Mauersberger, Stephan; Wang, Hui-Jie; Gaillardin, Claude; Barth, Gerold; Nicaud, Jean-Marc [Reprint author]
CORPORATE SOURCE: Laboratoire de Microbiologie et de Genetique Moleculaire, Institut National Agronomique Paris-Grignon, F-78850, Thiverval-Grignon, France
jean-marc.nicaud@grignon.inra.fr
SOURCE: Journal of Bacteriology, (September, 2001) Vol. 183, No. 17, pp. 5102-5109. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 5 Sep 2001
Last Updated on STN: 22 Feb 2002

AB Tagged mutants affected in the degradation of hydrophobic compounds (HC) were generated by insertion of a zeta-URA3 mutagenesis cassette (MTC) into the genome of a zeta-free and ura3 deletion-containing strain of Yarrowia lipolytica. MTC integration occurred predominantly at random by nonhomologous recombination. A total of 8,600 Ura+ **transformants** were tested by replica plating for (i) growth on minimal media with alkanes of different chain lengths (decane, dodecane, and hexadecane), oleic acid, tributyrin, or ethanol as the C source and (ii) colonial defects on different glucose-containing media (YPD, YNBD, and YNBcas). A total of 257 mutants were obtained, of which about 70 were affected in HC degradation, representing different types of non-alkane-utilizing (Alk-) mutants (phenotypic classes alkA to alkE) and tributyrin degradation mutants. Among Alk- mutants, growth defects depending on the alkane chain length were observed (alkAa to alkAc). Furthermore, mutants defective in yeast-hypha transition and ethanol utilization and selected auxotrophic mutants were isolated. **Flanking** borders of the integrated MTC were sequenced to identify the disrupted genes. Sequence analysis indicated that the MTC was integrated in the LEU1 locus in N083, a leucine-auxotrophic mutant, in the isocitrate dehydrogenase gene of N156 (alkE leaky), in the thioredoxin reductase gene in N040 (alkAc), and in a peroxine gene (PEX14) in N078 (alkD). This indicates that MTC integration is a powerful tool for generating and analyzing tagged mutants in Y. lipolytica.

L28 ANSWER 16 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:648546 CAPLUS
DOCUMENT NUMBER: 141:169002

TITLE: Protein and cDNA sequences of a novel human protooncogene HPP1, and use in cancer diagnosis and therapy
INVENTOR(S): Kim, Jin Woo
PATENT ASSIGNEE(S): S. Korea
SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004067562	A1	20040812	WO 2004-KR137	20040127

W: AE, AE, AG, AL, AL, AM, AM, AM, AT, AT, AU, AZ, AZ, BA, BB, BG, BG, BR, BR, BW, BY, BY, BZ, BZ, CA, CH, CN, CN, CO, CO, CR, CR, CU, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EC, EE, EE, EG, ES, ES, FI, FI, GB, GD, GE, GE, GH, GM, HR, HR, HU, HU, ID, IL, IN, IS, JP, JP, KE, KE, KG, KG, KP, KP, KP, KZ, KZ, KZ, LC, LK, LR, LS, LS, LT, LU, LV, MA, MD, MD, MG, MK, MN, MW, MX, MX, MZ, MZ, NA, NI, NI, NO

PRIORITY APPLN. INFO.: KR 2003-5185 A 20030127

AB The present invention relates to a novel proto-oncogene HPP1 (Human proto-oncogene 1), which is **non-homologous** to existing oncogenes and the protein encoded by the said oncogene. This novel proto-oncogene can be advantageously used in diagnosing of various cancers; in construction of **transformed** animals; and in anti-sense gene therapy.The present invention relates to a novel proto-oncogene HPP1 (Human proto-oncogene 1), which is **non-homologous** to existing oncogenes and the protein encoded by the said oncogene. This novel proto-oncogene can be advantageously used in diagnosing of various cancers; in construction of **transformed** animals; and in anti-sense gene therapy.

L28 ANSWER 17 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:142863 CAPLUS
DOCUMENT NUMBER: 136:195270
TITLE: Bacillus **transformation** and construction of mutant libraries
INVENTOR(S): Diaz-Torres, Maria R.; Schellenberger, Volker; Selifonova, Olga V.; Morrison, Thomas B.; Lee, Edwin W.
PATENT ASSIGNEE(S): Genencor International, Inc., USA
SOURCE: PCT Int. Appl., 48 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002014490	A2	20020221	WO 2001-US25166	20010810
WO 2002014490	A3	20030206		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,

DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA 2418317	AA	20020221	CA 2001-2418317	20010810
AU 2001079254	A5	20020225	AU 2001-79254	20010810
US 2002182734	A1	20021205	US 2001-927161	20010810
EP 1309677	A2	20030514	EP 2001-957519	20010810

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRIORITY APPLN. INFO.:	US 2000-224948P	P	20000811
	WO 2001-US25166	W	20010810

AB The present invention provides methods for building DNA constructs in vitro, **transforming** such constructs into competent Bacillus strains with good efficiency, and generating populations of mutants. Also provided is a method to assemble DNA constructs in situ. The invention also relates to methods for randomly mutagenizing a large DNA fragment, or the signal sequence, with an antibiotic marker and homologous DNA on either side of subtilisin gene. The invention also shows that the efficiency of **transformation** is increased by adding **non -homologous flanks** to the **transforming** DNA. The invention further relates to methods for performing site-directed mutagenesis on the gene of interest and directly **transform** Bacillus strains with the mutagenized DNA.

L28 ANSWER 18 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER:	1996:421349 CAPLUS
DOCUMENT NUMBER:	125:134553
TITLE:	Characterization of promoters and stable transfection by homologous and nonhomologous recombination in Plasmodium falciparum
AUTHOR(S):	Crabb, Brendan S.; Cowman, Alan F.
CORPORATE SOURCE:	Walter and Eliza Hall Institute Medical Research, Melbourne, 3050, Australia
SOURCE:	Proceedings of the National Academy of Sciences of the United States of America (1996), 93(14), 7289-7294 CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER:	National Academy of Sciences
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB Genetic studies of the protozoan parasite Plasmodium falciparum have been severely limited by the inability to introduce or modify genes. In this paper we describe a system of stable transfection of P. falciparum using a Toxoplasma gondii dihydrofolate reductase-thymidylate synthase gene, modified to confer resistance to pyrimethamine, as a selectable marker. This gene was placed under the transcriptional control of the P. falciparum calmodulin gene **flanking** sequences. Transfected parasites generally maintained plasmids episomally while under selection; however, parasite clones containing integrated forms of the plasmid were obtained. Integration occurred by both homologous and nonhomologous recombination. In addition to the **flanking** sequence of the P. falciparum calmodulin gene, the 5' sequences of the P. falciparum and P. chabaudi dihydrofolate reductase-thymidylate synthase genes were also shown to be transcriptionally active in P. falciparum. The minimal 5' sequence that possessed significant transcriptional activity was determined for each gene and short sequences containing important transcriptional control elements were identified. These sequences will provide considerable flexibility in the future construction of plasmid vectors to be used for the expression of foreign genes or for the deletion or modification of P. falciparum genes of interest.

L28 ANSWER 19 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER:	1993:618943 CAPLUS
DOCUMENT NUMBER:	119:218943

TITLE: Characterization of two identical independent **non-homologous** integration sites in mouse embryonic stem cells
AUTHOR(S): Sutherland, Helen F.; Lovell-Badge, Robin H.; Jackson, Ian J.
CORPORATE SOURCE: MRC Hum. Genet. Unit, West. Gen. Hosp., Edinburgh, EH4 2XU, UK
SOURCE: Gene (1993), 131(2), 265-8
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English

AB On anal. of 46 Geneticin-resistant (GtR) cell lines, derived by electroporation of mouse embryonic stem (ES) cells with a promoterless neo vector, the authors observed that in two independently derived cell lines, the vector had integrated into the same locus. The sequence **flanking** the vector integration site in both cell lines was cloned and sequenced. The vector had integrated into a 3 to 6-bp region in both cell lines. No homol. is observed between the integration site sequence and the vector sequence.

L28 ANSWER 20 OF 21 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-273717 [24] WPIDS
DOC. NO. CPI: C2000-083633
TITLE: **Non-homologous transformation** of Yarrowia comprises **transforming** a Yarrowia strain lacking zeta sequences with a recombinant vector harboring a gene insert **flanked** by zeta sequences.
DERWENT CLASS: C06 D16
INVENTOR(S): GAILLARDIN, C; NICAUD, J M; PIGNEDE, G; NICAUD, J
PATENT ASSIGNEE(S): (INRG) INRA INST NAT RECH AGRONOMIQUE; (CNRS) CNRS CENT NAT RECH SCI
COUNTRY COUNT: 89
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
FR 2782733	A1	20000303	(200024)*		17
WO 2000012729	A1	20000309	(200025)	FR	
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9954275	A	20000321	(200031)		
EP 1108043	A1	20010620	(200135)	FR	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
US 6582951	B1	20030624	(200343)		
EP 1108043	B1	20040331	(200426)	FR	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
DE 69916081	E	20040506	(200434)		
ES 2219051	T3	20041116	(200477)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
FR 2782733	A1	FR 1998-10900	19980901
WO 2000012729	A1	WO 1999-FR2079	19990901
AU 9954275	A	AU 1999-54275	19990901

EP 1108043	A1	EP 1999-940267	19990901
		WO 1999-FR2079	19990901
US 6582951	B1	WO 1999-FR2079	19990901
		US 2001-786048	20010427
EP 1108043	B1	EP 1999-940267	19990901
		WO 1999-FR2079	19990901
DE 69916081	E	DE 1999-616081	19990901
		EP 1999-940267	19990901
		WO 1999-FR2079	19990901
ES 2219051	T3	EP 1999-940267	19990901

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9954275	A	Based on	WO 2000012729
EP 1108043	A1	Based on	WO 2000012729
US 6582951	B1	Based on	WO 2000012729
EP 1108043	B1	Based on	WO 2000012729
DE 69916081	E	Based on	EP 1108043
		Based on	WO 2000012729
ES 2219051	T3	Based on	EP 1108043

PRIORITY APPLN. INFO: FR 1998-10900 19980901
AN 2000-273717 [24] WPIDS
AB FR 2782733 A UPAB: 20000522
NOVELTY - Method for integrating a gene (I) into the genome of a Yarrowia strain comprises **transforming** a Yarrowia strain lacking zeta sequences with a recombinant vector harboring a (I)-containing insert **flanked** by zeta sequences.
DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a **transformed** Yarrowia cell obtainable by the method.
USE - The method can be used e.g. to produce lipase-overexpressing **transformants** of Yarrowia lipolytica.
ADVANTAGE - Unlike methods involving **transformation** of Yarrowia strains having zeta sequences, which yields **transformants** with multiple tandem copies of the integrated sequence, **transformation** of Yarrowia strains lacking zeta sequences yields **transformants** with multiple dispersed copies of the integrated sequence.
Dwg.0/4

L28 ANSWER 21 OF 21 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 1993-094010 [11] WPIDS
DOC. NO. CPI: C1993-041627
TITLE: Purposive genetic modification of Ashbya (A) gossypii - by vectors containing insertable DNA within A. gossypii gene region, pref. from transcription elongation factor, useful in riboflavin production.
DERWENT CLASS: B04 D15
INVENTOR(S): KURTH, R; PHILIPPSEN, P; STEINER, S; WENDLAND, J; WRIGHT, M; WRIGHT, M C
PATENT ASSIGNEE(S): (BADI) BASF AG
COUNTRY COUNT: 19
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9304180	A1	19930304	(199311)*	GE	49
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL SE					
W: CA JP US					
EP 599945	A1	19940608	(199422)	GE	

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L14           54 E1-E4
L15           23 DUP REM L14 (31 DUPLICATES REMOVED)
L16            2 TRANSFORM? AND L15
L17            0 L3 AND L5
L18      1447160 TRANSFORM?
L19          470 L3 AND L18
L20            0 L19 AND L5
L21            5 L19 AND L10
L22            2 DUP REM L21 (3 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 11:34:16 ON 11 MAR 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 11:39:56 ON 11
     MAR 2005
L23           33 CONSTRUCT AND L19
L24           19 DUP REM L23 (14 DUPLICATES REMOVED)
L25           63 FLANK? AND L19
L26           27 DUP REM L25 (36 DUPLICATES REMOVED)
L27            6 L24 AND L26
L28           21 L26 NOT L27

=> logoff hold
COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                99.08     209.59

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)      SINCE FILE      TOTAL
                                                   ENTRY    SESSION
CA SUBSCRIBER PRICE                                -8.03      -9.49

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 11:49:45 ON 11 MAR 2005
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WEST Search History

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DATE: Friday, March 11, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR	
☐	L13	l9 and L12	144
☐	L12	l5 and L11	453
☐	L11	transform$.clm.	102599
☐	L10	l6 and L9	707
☐	L9	homologous with flank$	8328
☐	L8	homologous with stuffer	10
☐	L7	homogous with stuffer	0
☐	L6	transform$ and L5	1872
☐	L5	(non adj homologous or heterologous) with flank$	2041
☐	L4	transform$ and L3	5981
☐	L3	(non adj homologous or heterologous) with (construct or flank$)	6691
☐	L2	(non adj homologous or heterologous) same (construct or flank$)	11796
☐	L1	diaz-torres-maria.in.	5

END OF SEARCH HISTORY

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Friday, March 11, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT; PLUR=YES; OP=OR	
☐	L5	(non adj homologous same DNA same uptake)	9
☐	L4	(non adj homologous with DNA with uptake)	2
☐	L3	(initiat$ with DNA with uptake)	29
☐	L2	(initiate adj DNA adj uptake)	1
☐	L1	20020182734.pn.	1

END OF SEARCH HISTORY